

### III. AMENDMENT

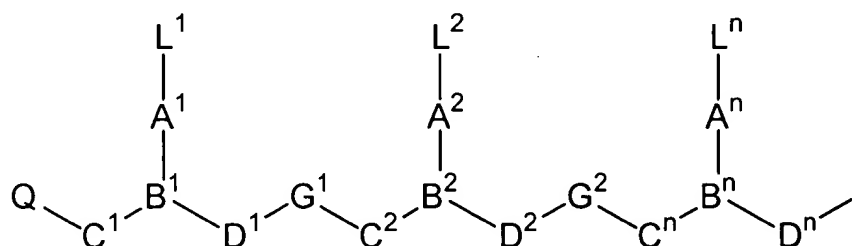
PLEASE ENTER THE FOLLOWING AMENDMENT WITHOUT PREJUDICE OR DISCLAIMER. Applicant reserves the right to file a divisional or continuation application to the originally filed claims.

1. (Previously Amended) A PNA probe of up to 30 subunits in length comprising a probing nucleobase sequence selected from the group consisting of: CTT-CAA-AGA-GGT-CCA-CGA (Seq. ID No. 1); AGG-GTT-CAA-CTG-TGT-GAC (Seq. ID No. 2); GAA-ACT-TCT-GAG-TGA-TGA (Seq. ID No. 3); CAG-TCA-TCG-CAG-AAA-ACT (Seq. ID No. 4); AGA-TTT-CAC-TGG-AAA-CGG (Seq. ID No. 5); GTT-ATG-GGA-AGG-TGA-TCC (Seq. ID No. 6); TCG-AGC-CGC-AGA-GTT-TAA (Seq. ID No. 7); CTA-TTT-AGC-GGG-CTT-GGA (Seq. ID No. 8); TAC-AAG-GGT-GTT-GCA-AAC (Seq. ID No. 9); CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT (Seq. ID No. 15); GGC-ATA-GCA-CAT-AAC-ATG (Seq. ID No. 16); AAT-CGT-CAT-CGA-ATG-AAT (Seq. ID No. 17); CAT-TGA-ACA-GAA-TTG-AAT (Seq. ID No. 18); GTT-TTC-AGG-GGA-AGA-TAT (Seq. ID No. 19); TGT-GCG-CCC-TCA-ACT-AAC (Seq. ID No. 20); GAA-GCT-TCA-TTG-GGA-TGT (Seq. ID No. 21); CCA-ATA-AAA-GCT-ACA-TAG-A (Seq. ID No. 22); GAA-AAA-GTT-TCT-GAC-ATT-GC (Seq. ID No. 23); TAG-TTG-AAG-GGC-ACA-TCA (Seq. ID No. 24); CAC-AAA-TAA-GAT-TCT-AAG-AAT (Seq. ID No. 25); TCA-AAA-GAA-TGC-TTC-AAC-AC (Seq. ID No. 26); ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27); GCT-GTT-TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-AGG-TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID No. 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-TCA-ACT-CAC-GGA (Seq. ID No. 32); CCT-CAC-AAA-GTA-GAA-ACT (Seq. ID No. 33); GAA-AAA-GCA-GTT-ACT-GAG (Seq. ID No. 34); TAA-TAA-TTA-GAC-GGA-ATC-AT (Seq. ID No. 35); TTA-CAG-GGC-ATT-GAA-GCC (Seq. ID No. 36); CAG-TTA-TGA-

AGC-AGT-CTC (Seq. ID No. 37); CAC-ACC-AGA-AAA-AGC-AGT (Seq. ID No. 38); AAG-GGT-AAA-CAC-TGT-GAG (Seq. ID No. 39); AGA-CAA-CGA-AAT-ATC-TTC-ATG (Seq. ID No. 40); CTA-GCA-GTA-TGA-GGT-CAA (Seq. ID No. 41); GCA-GAC-TTC-AGA-AAC-AGA (Seq. ID No. 42); GGC-CTC-AAA-GAC-GTT-TAA (Seq. ID No. 43); GTG-AAA-GTT-CCA-AGT-GAA (Seq. ID No. 44); GAG-TGC-TTT-GAA-GCC-TAC (Seq. ID No. 45); GAA-ACA-GCA-GAG-TTG-AAA (Seq. ID No. 46); TGC-AGA-GAT-CAC-AAC-GTG (Seq. ID No. 47); ACA-AAG-AAT-CAT-TCG-CAG (Seq. ID No. 48); AGT-GTT-AGA-AAA-CTG-CTC (Seq. ID No. 49); ACA-CGA-TTT-TGG-AAA-CAC (Seq. ID No. 119); CGA-AAC-ATC-ACT-GAG-AGT (Seq. ID No. 120); GGA-TGA-CAT-ATA-ATA-ACT-AG (Seq. ID No. 121); GAA-TTG-AAC-ATT-CAC-TTT-GA (Seq. ID No. 122); TAG-CTC-TGA-AGA-TTT-CGT (Seq. ID No. 123); GAG-ATG-TTT-CCG-AGA-ATG (Seq. ID No. 124); GTG-TAT-TCA-ACT-ACC-AGA (Seq. ID No. 125); ACA-TTT-CTG-TTA-CAG-AGC (Seq. ID No. 126); ATG-ACG-TAT-AAA-ATC-TAG-AG (Seq. ID No. 127); ACG-AAC-ACA-GTT-GAA-CCT (Seq. ID No. 128); CTC-ATA-AAA-ACC-AGA-AAG-AG (Seq. ID No. 129); CTG-TTC-AGA-GTA-ACA-TGA (Seq. ID No. 50); CCG-CTT-GGA-AAT-ACT-ACA (Seq. ID No. 51); GAA-ATG-GAA-ATA-TCT-CCC-C (Seq. ID No. 52); TCT-AGG-AGG-TCC-AAT-TAT (Seq. ID No. 53); GAA-TTC-CCA-AGT-GGA-TAT (Seq. ID No. 54); CTG-TAG-GTT-TAG-ATG-AAG (Seq. ID No. 55); AAG-GAG-TGT-TTC-CCA-ACT (Seq. ID No. 56); GGC-TTC-AAG-GCG-CTC-TAA (Seq. ID No. 57); GCA-GAG-ACT-TCA-AAG-TGC (Seq. ID No. 58); CAC-ACA-CAC-GGT-GGA-CCA (Seq. ID No. 59); CAA-AGG-GAA-TGT-TCC-ATT (Seq. ID No. 60); CAC-ATA-GCA-GTG-TTT-GAG (Seq. ID No. 61); CTC-AAG-GCG-GTC-CAA-TTA (Seq. ID No. 62); GAG-TCG-AAA-TGC-ACA-CAT (Seq. ID No. 63); TAC-CAA-GAG-GAA-TGT-TGC (Seq. ID No. 64); CAG-TTC-ATA-TGT-GCA-GTG (Seq. ID No. 130); GGA-ATA-TCG-TCA-CCT-AAA (Seq. ID No. 131); TGG-AGC-AAA-TTG-AAG-CCT (Seq. ID No. 132); TGG-AGC-ACA-TTT-ATG-CCT (Seq. ID No. 133); TGC-ATT-CTA-CTC-CCA-TAG (Seq. ID No. 134); ACA-CTC-TGT-TTC-TAA-AAT-CT (Seq. ID No. 135); GCA-GGC-GGA-TAT-TTA-GTA (Seq. ID No. 136); AGC-GAT-TTG-ATG-CCA-ACA (Seq. ID No. 137); TTG-CAA-ACG-GGG-TTT-CTT (Seq. ID No. 138); CTT-TCA-TGC-TAG-ACA-GAA (Seq.

ID No. 139); CAA-AAA-AGT-TAC-TGA-GAA-C (Seq. ID No. 140); AAA-ATG-CCA-CAG-CAA-GAG (Seq. ID No. 141); GTT-TGA-AAA-CAC-ACT-GTT-TG (Seq. ID No. 142); ATA-TGG-ACC-TGT-TTG-AGG (Seq. ID No. 143); CAT-TGA-ATG-CTA-GAC-GGA (Seq. ID No. 144); ACG-GGA-TGC-AAT-ATA-AAA (Seq. ID No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No. 66); AAG-GTT-TGT-ACT-GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-GGT-GAA-AAA (Seq. ID No. 68); ACT-AAC-TGT-GCT-GAA-CAT (Seq. ID No. 69); CCC-ATG-AAT-GCG-AGA-TAG (Seq. ID No. 70); ATG-ATG-AAA-AAG-GTA-ATA (Seq. ID No. 145); CAT-TCT-CAG-AAC-TGT-TTG (Seq. ID No. 146); AAC-TGA-ACG-CAC-AGA-TGA (Seq. ID No. 71); GGC-TAA-TCT-TTG-AAA-TTG-AAA (Seq. ID No. 72); AGG-TGG-ATA-ATT-GGC-CCT (Seq. ID No. 73); TGA-AGT-CCA-AAA-AAG-CAC (Seq. ID No. 74); CTT-AGA-CAT-GGA-AAT-ATC (Seq. ID No. 75); AAG-GGG-TCT-AAC-TAA-TCA (Seq. ID No. 76); GTA-GTT-GTT-GAG-AAT-GAT (Seq. ID No. 77); AAC-TTC-CCA-GAA-CTA-CAC (Seq. ID No. 78); ATT-CTT-GAA-ATG-GAA-CAC (Seq. ID No. 79); CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq. ID No. 81); GAA-ATT-TCC-TGT-TGA-CAG-A (Seq. ID No. 82); GTT-TGA-AAG-CTG-AAC-TAT-G (Seq. ID No. 83); TCC-TGT-AAT-GTT-CGA-CAG (Seq. ID No. 84); TCA-TAG-AAC-GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-AAG-GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID No. 87); GAG-TTG-AAT-AGA-GGC-AAC (Seq. ID No. 88); GGC-CAA-ATG-TAG-AAA-AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No. 92); GAA-TAC-TGA-GTA-AGT-TCT-TTG (Seq. ID No. 93); AAC-TGC-ACA-AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT (Seq. ID No. 95); CCA-GTT-GGA-GAT-TTC-AAT (Seq. ID No. 96); GAA-GCC-TGC-CAG-TGG-ATA (Seq. ID No. 97); TAC-AGC-ATT-CTG-GAA-ACC (Seq. ID No. 98); CCA-GAC-ACT-GCG-TAG-TGA (Seq. ID No. 99); ATA-TAA-TGC-TAG-AGG-GAG (Seq. ID No. 100); AAA-AAC-AAG-ACA-AAC-TCG (Seq. ID No. 101); ATT-TCA-GCT-GAC-TAA-ACA (Seq. ID No. 102); AAC-GAA-TTA-TGG-TCA-CAT (Seq. ID No. 103); GGT-GAC-GAC-TGA-GTT-TAA (Seq. ID No. 104); TTT-GGA-CCA-CTC-TGT-GGC (Seq. ID No. 105); AAC-GGG-ATA-ACT-GCA-CCT

(Seq. ID No. 106); TTT-GTG-GTT-TGT-GGT-GGA (Seq. ID No. 107); AGG-GAA-TAG-CTT-CAT-AGA (Seq. ID No. 108); ATC-ACG-AAG-AAG-GTT-CTG (Seq. ID No. 109); CCG-AAG-ATG-TCT-TTG-GAA (Seq. ID No. 110); AAA-GAG-GTC-TAC-ATG-TCC (Seq. ID No. 111); TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115); ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116); GCA-CTT-ACC-GGC-CTA-AG (Seq. ID No. 117); CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118); ACA-GAA-CTA-AAC-CAT-CGT (Seq. ID No. 147); TAG-GCC-AGC-TTG-GAG-GAT (Seq. ID No. 148); CTA-GCT-GGG-AGG-ATT-T (Seq. ID No. 149); TGT-GCC-TCA-ACT-GAC-A (Seq. ID No. 150); TGC-TTT-GGG-ATG-TTT-CAA (Seq. ID No. 151); GCA-ATG-TCA-GAA-CTT-TTT-TC (Seq. ID No. 152); CCG-AAA-GAA-ATT-TGT-GGG (Seq. ID No. 153); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 154); TCA-AGG-CGA-TCG-AAA-TGT (Seq. ID No. 155); GAG-ACA-CAT-ATC-ACC-AAC (Seq. ID No. 156); CAG-AAA-TTT-CTT-TCG-GAT-A (Seq. ID No. 157); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 158) and AGC-CAA-AGG-AGT-TGA-ACA (Seq. ID No. 159), or the complement to any of the foregoing sequences; wherein said PNA probe has the formula:



wherein,

n is at least 2,

each of  $L^1$ - $L^n$  is independently selected from the group consisting of hydrogen, hydroxy,  $(C_1-C_4)$ alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of  $C^1$ - $C^n$  is  $(CR^6R^7)_y$ , where  $R^6$  is hydrogen and  $R^7$  is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or  $R^6$  and  $R^7$  are independently selected from the group consisting of hydrogen,

(C<sub>2</sub>-C<sub>6</sub>)alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C<sub>1</sub>-C<sub>6</sub>)alkoxy, (C<sub>1</sub>-C<sub>6</sub>)alkylthio, NR<sup>3</sup>R<sup>4</sup> and SR<sup>5</sup>, where R<sup>3</sup> and R<sup>4</sup> are as defined above, and R<sup>5</sup> is hydrogen, (C<sub>1</sub>-C<sub>6</sub>)alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C<sub>1</sub>-C<sub>6</sub>)alkyl, or R<sup>6</sup> and R<sup>7</sup> taken together complete an alicyclic or heterocyclic system;

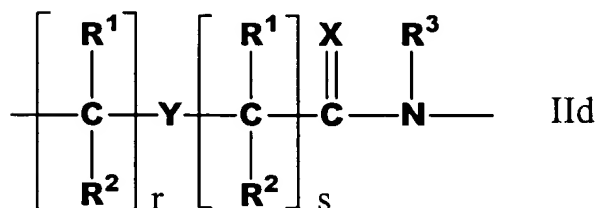
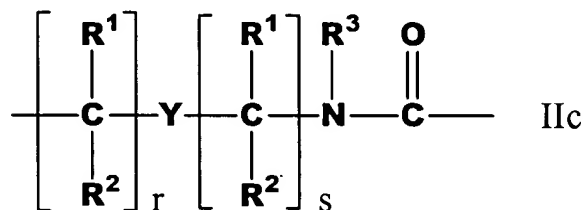
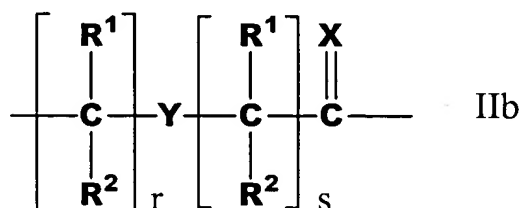
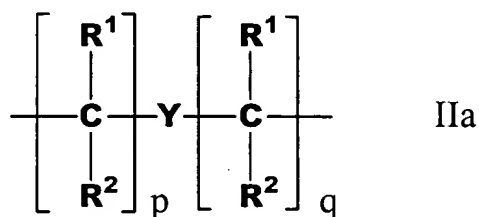
each of D<sup>1</sup>-D<sup>n</sup> is (CR<sup>6</sup>R<sup>7</sup>)<sub>z</sub> where R<sup>6</sup> and R<sup>7</sup> are as defined above;

each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

each of G<sup>1</sup>-G<sup>n-1</sup> is -NR<sup>3</sup>CO-, -NR<sup>3</sup>CS-, -NR<sup>3</sup>SO- or -NR<sup>3</sup>SO<sub>2</sub>-, in either orientation, where R<sup>3</sup> is as defined above;

each of A<sup>1</sup>-A<sup>n</sup> and B<sup>1</sup>-B<sup>n</sup> are selected such that:

- (a) A is a group of the formula (IIa), (IIb), (IIc), or (IId), and B is N or R<sup>3</sup>N'; or
- (b) A is a group of formula (IId) and B is CH;



where:

X is O, S, Se,  $\text{NR}^3$ ,  $\text{CH}_2$  or  $\text{C}(\text{CH}_3)_2$ ;

Y is a single bond, O, S or  $\text{NR}^4$ ;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each  $\text{R}^1$  and  $\text{R}^2$  is independently selected from the group consisting of hydrogen,  $(\text{C}_1\text{-C}_4)\text{alkyl}$  which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each  $\text{R}^3$  and  $\text{R}^4$  is independently selected from the group consisting of hydrogen,  $(\text{C}_1\text{-C}_4)\text{alkyl}$ , hydroxy- or alkoxy- or alkylthio-substituted  $(\text{C}_1\text{-C}_4)\text{alkyl}$ , hydroxy, alkoxy, alkylthio and amino;

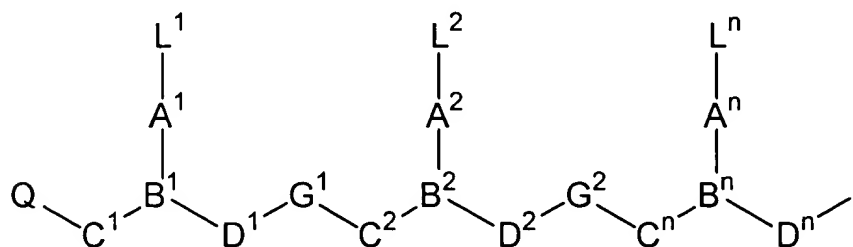
Q is  $-\text{CO}_2\text{H}$ ,  $-\text{CONR}'\text{R}''$ ,  $-\text{SO}_3\text{H}$  or  $-\text{SO}_2\text{NR}'\text{R}''$  or an activated derivative of  $-\text{CO}_2\text{H}$  or  $-\text{SO}_3\text{H}$ ; and

I is  $-\text{NHR}'''\text{R}''''$  or  $-\text{NR}'''\text{C}(\text{O})\text{R}''''$ , where  $\text{R}'$ ,  $\text{R}''$ ,  $\text{R}'''$  and  $\text{R}''''$  are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

(Claims 2-3, Canceled)

4. (Original) The probe of claim 1, wherein the probe is unlabeled.
5. (Original) The probe of claim 1, wherein the probe is labeled with at least one detectable moiety.
6. (Original) The probe of claim 5, wherein the detectable moiety or moieties are selected from the group consisting of: a dextran conjugate, a branched nucleic acid detection system, a chromophore, a fluorophore, a spin label, a radioisotope, an enzyme, a hapten, an acridinium ester and a chemiluminescent compound.

7. (Original) The probe of claim 1, wherein the probe is labeled with at least two independently detectable moieties.
8. (Original) The probe of claim 7, wherein the two or more independently detectable moieties are independently detectable fluorophores.
9. (Original) The probe of claim 1, wherein the probe is support bound.
10. (Currently Amended) A probe set comprising at least one PNA probes of up to 30 subunits in length wherein said PNA probe or probes have the formula:



wherein,

n is at least 2,

each of  $L^1$ - $L^n$  is independently selected from the group consisting of hydrogen, hydroxy,  $(C_1-C_6)$ alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of  $C^1$ - $C^n$  is  $(CR^6R^7)_y$ , where  $R^6$  is hydrogen and  $R^7$  is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or  $R^6$  and  $R^7$  are independently selected from the group consisting of hydrogen,  $(C_2-C_6)$ alkyl, aryl, aralkyl, heteroaryl, hydroxy,  $(C_1-C_6)$ alkoxy,  $(C_1-C_6)$ alkylthio,  $NR^3R^4$  and  $SR^5$ , where  $R^3$  and  $R^4$  are as defined above, and  $R^5$  is hydrogen,  $(C_1-C_6)$ alkyl, hydroxy-, alkoxy-, or alkylthio- substituted  $(C_1-C_6)$ alkyl, or  $R^6$  and  $R^7$  taken together complete an alicyclic or heterocyclic system;

each of  $D^1$ - $D^n$  is  $(CR^6R^7)_z$ , where  $R^6$  and  $R^7$  are as defined above;

each of y and z is zero or an integer from 1 to 10, the sum  $y+z$  being greater than 2 but not more than 10;

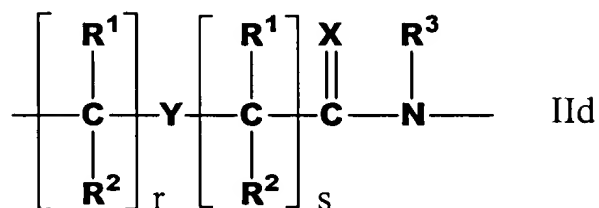
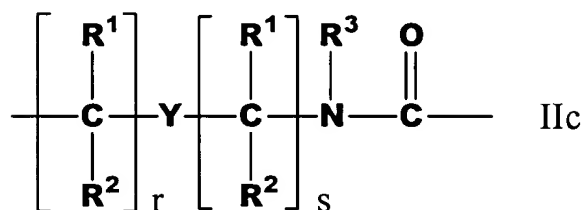
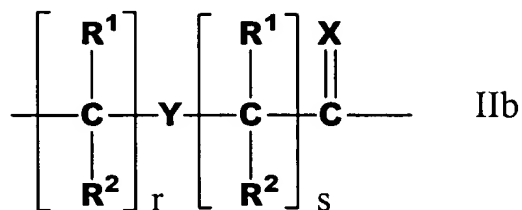
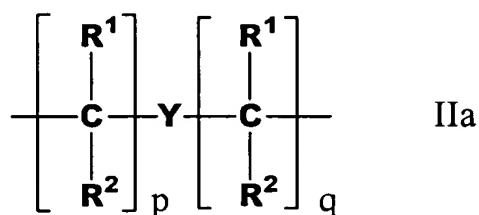
each of  $G^1-G^{n-1}$  is  $-NR^3CO-$ ,  $-NR^3CS-$ ,  $-NR^3SO-$  or  $-NR^3SO_2-$ , in either orientation,

where  $R^3$  is as defined above;

each of  $A^1-A^n$  and  $B^1-B^n$  are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (IIId), and B is N or  $R^3N^+$ ; or

(b) A is a group of formula (IIId) and B is CH;



where:

X is O, S, Se,  $NR^3$ ,  $CH_2$  or  $C(CH_3)_2$ ;

Y is a single bond, O, S or  $NR^4$ ;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;



each  $R^1$  and  $R^2$  is independently selected from the group consisting of hydrogen,  $(C_1-C_4)$ alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each  $R^3$  and  $R^4$  is independently selected from the group consisting of hydrogen,  $(C_1-C_4)$ alkyl, hydroxy- or alkoxy- or alkylthio-substituted  $(C_1-C_4)$ alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is  $-\text{CO}_2\text{H}$ ,  $-\text{CONR}'\text{R}''$ ,  $-\text{SO}_3\text{H}$  or  $-\text{SO}_2\text{NR}'\text{R}''$  or an activated derivative of  $-\text{CO}_2\text{H}$  or  $-\text{SO}_3\text{H}$ ; and

I is  $-\text{NHR}'''\text{R}''''$  or  $-\text{NR}'''\text{C(O)R}''''$ , where  $R'$ ,  $R''$ ,  $R'''$  and  $R''''$  are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids; and wherein:  
~~the one or more PNA probes of the set specific for detecting human chromosome X comprise a probing nucleobase sequence selected from the group consisting of:~~

~~CTT CAA AGA GGT CCA CGA (Seq. ID No. 1); AGG GTT CAA CTG TGT GAC (Seq. ID No. 2); GAA ACT TCT GAG TGA TGA (Seq. ID No. 3); CAG TCA TCG CAG AAA ACT (Seq. ID No. 4); AGA TTT CAC TGG AAA CGG (Seq. ID No. 5); GTT ATG GGA AGG TGA TCC (Seq. ID No. 6); TCG AGC CGC AGA GTT TAA (Seq. ID No. 7); CTA TTT AGC GGG CTT GGA (Seq. ID No. 8) and TAC AAG GGT GTT GCA AAC (Seq. ID No. 9), or the complement to any of the foregoing sequences;~~

~~the one or more of the PNA probes of the set is specific for detecting human chromosome Y and comprises a probing nucleobase sequence selected from the group consisting of:~~

~~CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT~~

(Seq. ID No. 15) and GGC-ATA-GCA-CAT-AAC-ATG (Seq. ID No. 16), or the complement to any of the foregoing sequences; the one or more PNA probes of the set specific for detecting human chromosome 1 comprise a probing nucleobase sequence, selected from the group consisting of:

~~AAT CGT CAT CGA ATG AAT (Seq. ID No. 17) and CAT TGA ACA GAA TTG AAT (Seq. ID No. 18), or the complement to any of the foregoing sequences;~~

the one or more PNA probes of the set specific for detecting human chromosome 2 comprise a probing nucleobase sequence selected from the group consisting of:

~~GTT TTC AGG GGA AGA TAT (Seq. ID No. 19); TGT GCG CCC TCA ACT AAC (Seq. ID No. 20); GAA GCT TCA TTG GGA TGT (Seq. ID No. 21); CCA ATA AAA GCT ACA TAG A (Seq. ID No. 22); GAA AAA GTT TCT GAC ATT GC (Seq. ID No. 23); TAG TTG AAG GGC ACA TCA (Seq. ID No. 24); CAC AAA TAA GAT TCT AAG AAT (Seq. ID No. 25) and TCA AAA GAA TGC TTC AAC AC (Seq. ID No. 26), or the complement to any of the foregoing sequences;~~

the one or more PNA probes of the set specific for detecting human chromosome 3 comprise a probing nucleobase sequence selected from the group consisting of:

~~ATA ATT AGA CCG GAA TCA T (Seq. ID No. 27); GCT GTT TTC TAA AGG AAA G (Seq. ID No. 28); AAG ACT TCA AAG AGG TCC (Seq. ID No. 29); TTT GTC AAG AAT TAT AAG AAG (Seq. ID No. 30); CAA GAT TGC TTT TAA TGG (Seq. ID No. 31); TGT GTA TCA ACT CAC GGA (Seq. ID No. 32); CCT CAC AAA GTA GAA ACT (Seq. ID No. 33); GAA AAA GCA GTT ACT GAG (Seq. ID No. 34); TAA TAA TTA GAC GGA ATC AT (Seq. ID No. 35); TTA CAG GGC ATT GAA CCC (Seq. ID No. 36); CAG TTA TGA AGC AGT CTC (Seq. ID No. 37);~~

~~CAC ACC AGA AAA AGC AGT (Seq. ID No. 38); AAG GGT AAA CAC TGT GAG (Seq. ID No. 39); AGA CAA CGA AAT ATC TTC ATG (Seq. ID No. 40); CTA GCA GTA TGA GGT CAA (Seq. ID No. 41); GCA GAC TTC AGA AAC AGA (Seq. ID No. 42); GGC CTC AAA GAC GTT TAA (Seq. ID No. 43); GTG AAA GTT CCA AGT GAA (Seq. ID No. 44); GAG TGC TTT GAA GCC TAC (Seq. ID No. 45); GAA ACA GCA GAG TTG AAA (Seq. ID No. 46); TGC AGA GAT CAC AAC GTG (Seq. ID No. 47); ACA AAG AAT CAT TCG CAG (Seq. ID No. 48); and AGT GTT AGA AAA CTG CTC (Seq. ID No. 49), or the complement to any of the foregoing sequences;~~

~~the one or more PNA probes of the set specific for detecting human chromosome 4 comprise a probing nucleobase sequence selected from the group consisting of:~~

~~ACA CGA TTT TGG AAA CAC (Seq. ID No. 119); CGA AAC ATC ACT GAG AGT (Seq. ID No. 120); GGA TGA CAT ATA ATA ACT AG (Seq. ID No. 121); GAA TTG AAC ATT CAC TTT GA (Seq. ID No. 122); TAG CTC TGA AGA TTT CGT (Seq. ID No. 123); GAG ATG TTT CCG AGA ATG (Seq. ID No. 124); GTG TAT TCA ACT ACC AGA (Seq. ID No. 125); ACA TTT CTG TTA CAG AGC (Seq. ID No. 126); ATG ACG TAT AAA ATC TAG AG (Seq. ID No. 127); ACG AAC ACA GTT GAA CCT (Seq. ID No. 128); and CTC ATA AAA ACC AGA AAG AG (Seq. ID No. 129), or the complement to any of the foregoing sequences;~~

~~the one or more PNA probes of the set specific for detecting human chromosome 6 comprise a probing nucleobase sequence selected from the group consisting of:~~

~~CTG TTC AGA GTA ACA TGA (Seq. ID No. 50); CCG CTT GGA AAT ACT ACA (Seq. ID No. 51); GAA ATG GAA ATA TCT CCC C (Seq. ID No. 52); TCT AGG AGG TCC AAT TAT~~

(Seq. ID No. 53); ~~GAA TTC CCA AGT GGA TAT (Seq. ID No. 54); CTG TAG GTT TAG ATG AAG (Seq. ID No. 55); AAG GAG TGT TTC CCA ACT (Seq. ID No. 56); GGC TTC AAG GCG CTC TAA (Seq. ID No. 57); GCA GAG ACT TCA AAG TGC (Seq. ID No. 58); CAC ACA CAC GGT GGA CCA (Seq. ID No. 59); CAA AGG GAA TGT TCC ATT (Seq. ID No. 60); CAC ATA GCA GTG TTT GAG (Seq. ID No. 61); CTC AAG GCG GTC CAA TTA (Seq. ID No. 62); GAG TCG AAA TGC ACA CAT (Seq. ID No. 63) and TAC CAA GAG GAA TGT TGC (Seq. ID No. 64), or the complement to any of the foregoing sequences;~~  
the one or more PNA probes of the set specific for detecting human chromosome 7 comprise a probing nucleobase sequence selected from the group consisting of:

~~CAG TTC ATA TGT GCA GTG (Seq. ID No. 130); GGA ATA TCG TCA CCT AAA (Seq. ID No. 131); TGG AGC AAA TTG AAG CCT (Seq. ID No. 132); TGG AGC ACA TTT ATG CCT (Seq. ID No. 133); TGC ATT CTA CTC CCA TAG (Seq. ID No. 134); ACA CTC TGT TTC TAA AAT CT (Seq. ID No. 135); GCA GGC GGA TAT TTA GTA (Seq. ID No. 136); AGC GAT TTG ATG CCA ACA (Seq. ID No. 137); TTG CAA ACG GGG TTT CTT (Seq. ID No. 138); CTT TCA TGC TAG ACA GAA (Seq. ID No. 139); CAA AAA AGT TAC TGA GAA C (Seq. ID No. 140); AAA ATG CCA CAG CAA GAG (Seq. ID No. 141); GTT TGA AAA CAC ACT GTT TG (Seq. ID No. 142); ATA TGG ACC TGT TTG AGG (Seq. ID No. 143); and CAT TGA ATG CTA GAC GGA (Seq. ID No. 144), or the complement to any of the foregoing sequences;~~  
the one or more PNA probes of the set specific for detecting human chromosome 8 comprise a probing nucleobase sequence selected from the group consisting of:

~~ACG-GGA-TGC-AAT-ATA-AAA (Seq. ID No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No. 66); AAG-GTT-TGT-ACT-GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-GGT-GAA-AAA (Seq. ID No. 68); ACT-AAC-TGT-GCT-GAA-CAT (Seq. ID No. 69) and CCC-ATG-AAT-GCG-AGA-TAG (Seq. ID No. 70), or the complement to any of the foregoing sequences;~~

~~the one or more PNA probes of the set specific for detecting human chromosome 9 comprise a probing nucleobase sequence selected from the group consisting of:~~

~~ATG-ATG-AAA-AAG-GTA-ATA (Seq. ID No. 145) and CAT-TCT-CAG-AAC-TGT-TTG (Seq. ID No. 146), or the complement to any of the foregoing sequences;~~

~~the one or more PNA probes of the set specific for detecting human chromosome 10 comprise a probing nucleobase sequence selected from the group consisting of:~~

~~— AAC-TGA-ACG-CAC-AGA-TGA (Seq. ID No. 71); GGC-TAA-TCT-TTG-AAA-TTG-AAA (Seq. ID No. 72); AGG-TGG-ATA-ATT-GGC-CCT (Seq. ID No. 73); TGA-AGT-CCA-AAA-AAG-CAC (Seq. ID No. 74); CTT-AGA-CAT-GGA-AAT-ATC (Seq. ID No. 75); AAG-GGG-TCT-AAC-TAA-TCA (Seq. ID No. 76) and GTA-GTT-GTT-GAG-AAT-GAT (Seq. ID No. 77), or the complement to any of the foregoing sequences;~~

~~the one or more PNA probes of the set specific for detecting human chromosome 11 comprise a probing nucleobase sequence selected from the group consisting of:~~

~~AAC-TTC-CCA-GAA-CTA-CAC (Seq. ID No. 78); ATT-CTT-GAA-ATG-GAA-CAC (Seq. ID No. 79); CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq. ID No. 81); GAA-ATT-TCC-TGT-TGA-CAG-A (Seq. ID No. 82) and GTT-TGA-AAG-CTG-AAC-TAT-G (Seq. ID No. 83), or the complement to any of the foregoing sequences;~~

the one or more PNA probes of the set specific for detecting human chromosome 12 comprise a probing nucleobase sequence, selected from the group consisting of:

~~TCC TGT AAT GTT CGA CAG (Seq. ID No. 84); TCA TAG AAC GCT AGA AAG (Seq. ID No. 85); ACC TTT CTT TTG ATG AAG GA (Seq. ID No. 86); CAA ATA TCA CAA AAA GAG GG (Seq. ID No. 87); GAG TTG AAT AGA GGC AAC (Seq. ID No. 88); GGC CAA ATG TAG AAA AGG (Seq. ID No. 89); GCG TTC AAC TCA AGG TGT (Seq. ID No. 90); TGT CCT TTA GAC AGA GCA (Seq. ID No. 91); TGA GAC CAA ATG TAC AAA AG (Seq. ID No. 92); GAA TAC TGA GTA AGT TCT TTG (Seq. ID No. 93); AAC TGC ACA AAT AGG GTG (Seq. ID No. 94); TGG AGA CAC TGT GTT TGT (Seq. ID No. 95) and CCA GTT GGA GAT TTC AAT (Seq. ID No. 96), or the complement of any of the foregoing sequences;~~

the one or more PNA probes of the set specific for detecting human chromosome 16 comprise a probing nucleobase sequence selected from the group consisting of:

~~GAA GCC TGC CAG TGG ATA (Seq. ID No. 97); TAC AGC ATT CTG GAA ACC (Seq. ID No. 98); CCA GAC ACT GCG TAG TGA (Seq. ID No. 99); ATA TAA TGC TAG AGG GAG (Seq. ID No. 100) and AAA AAC AAG ACA AAC TCG (Seq. ID No. 101), or the complement to any of the foregoing sequences;~~

the one or more PNA probes of the set specific for detecting human chromosome 17 comprise a probing nucleobase sequence selected from the group consisting of:

~~ATT TCA GCT GAC TAA ACA (Seq. ID No. 102); AAC GAA TTA TGG TCA CAT (Seq. ID No. 103); GGT GAC GAC TGA GTT TAA (Seq. ID No. 104); TTT GGA CCA CTC TGT GGC (Seq. ID No. 105); AAC GGG ATA ACT GCA CCT (Seq. ID No. 106); TTT GTG GTT TGT GGT GGA (Seq. ID No. 107); AGG GAA~~

~~TAG CTT CAT AGA (Seq. ID No. 108); ATC ACG AAG AAG GTT CTG (Seq. ID No. 109); CCG AAG ATG TCT TTG GAA (Seq. ID No. 110) and AAA GAG GTC TAC ATG TCC (Seq. ID No. 111); or the complement to any of the foregoing sequences;~~  
the one or more PNA probes of the set specific for detecting human chromosome 18 comprise a probing nucleobase sequence selected from the group consisting of:

~~TTC CCG TAA CAA CTA TGC (Seq. ID No. 112); TCC CGT AAC AAC TAG GCA (Seq. ID No. 113); AAA AGG AGT GAT CCA ACC (Seq. ID No. 114); TCC CTT TGG TAG AGC AGG (Seq. ID No. 115); ATT TGA GAT GTG TGT ACT CA (Seq. ID No. 116); GCA CTT ACC GGC CTA AG (Seq. ID No. 117) and CTC AGA AAC TTA CTC GTG (Seq. ID No. 118) or the complement to any of the foregoing sequences;~~

the one or more PNA probes of the set specific for detecting human chromosome 20 comprise a probing nucleobase sequence selected from the group consisting of:

~~ACA GAA CTA AAC CAT CGT (Seq. ID No. 147); TAG GCC AGC TTG GAG GAT (Seq. ID No. 148); CTA GCT GGG AGG ATT T (Seq. ID No. 149); TGT GCC TCA ACT GAC A (Seq. ID No. 150); TGC TTT GGG ATG TTT CAA (Seq. ID No. 151); and GCA ATG TCA GAA CTT TTT TC (Seq. ID No. 152) or the complement to any of the foregoing sequences;~~

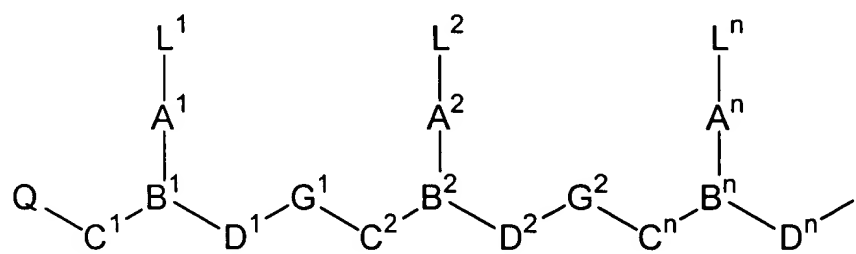
the one or more PNA probes of the set specific for detecting human chromosome 13/21 comprise a probing nucleobase sequence selected from the group consisting of:

~~CCG AAA GAA ATT TGT GGG (Seq. ID No. 153); GAA CAT GGC CTT TCA TAG (Seq. ID No. 154); TCA AGG CGA TCG AAA TGT (Seq. ID No. 155); GAG ACA CAT ATC ACC AAC (Seq. ID No. 156); CAG AAA TTT CTT TCG GAT A (Seq. ID No. 157); GAA CAT GGC CTT TCA TAG (Seq. ID No. 158) and AGC~~

~~CAA AGG AGT TGA ACA (Seq. ID No. 159), or the complement to any of the foregoing sequences.~~

(Claims 11-12; Canceled)

13. (Currently Amended) The probe set of claim 10, wherein the probe set comprises at least two probes and wherein two or more probes of the set are independently detectable.
14. (Original) The probe set of claim 13, wherein one or more of the independently detectable probes are labeled with two or more independently detectable moieties.
15. (Original) The probe set of claims 13, wherein the independently detectable probes are used to distinguish between human chromosomes X, Y, 1, 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 16, 17, 18 and 20, as well as 13/21 as a pair.
16. (Currently Amended; Withdrawn) A probe set comprising at least one PNA probes of ~~10~~ up to 30 subunits in length wherein said PNA probe or probes have the formula:



wherein,

n is at least 2,

each of L<sup>1</sup>-L<sup>n</sup> is independently selected from the group consisting of hydrogen, hydroxy, (C<sub>1</sub>-C<sub>4</sub>)alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;



each of C<sup>1</sup>-C<sup>n</sup> is (CR<sup>6</sup>R<sup>7</sup>), where R<sup>6</sup> is hydrogen and R<sup>7</sup> is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R<sup>6</sup> and R<sup>7</sup> are independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>6</sub>)alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C<sub>1</sub>-C<sub>6</sub>)alkoxy, (C<sub>1</sub>-C<sub>6</sub>)alkylthio, NR<sup>3</sup>R<sup>4</sup> and SR<sup>5</sup>, where R<sup>3</sup> and R<sup>4</sup> are as defined above, and R<sup>5</sup> is hydrogen, (C<sub>1</sub>-C<sub>6</sub>)alkyl, hydroxy-, alkoxy-, or alkylthio-substituted (C<sub>1</sub>-C<sub>6</sub>)alkyl, or R<sup>6</sup> and R<sup>7</sup> taken together complete an alicyclic or heterocyclic system;

each of D<sup>1</sup>-D<sup>n</sup> is (CR<sup>6</sup>R<sup>7</sup>), where R<sup>6</sup> and R<sup>7</sup> are as defined above;

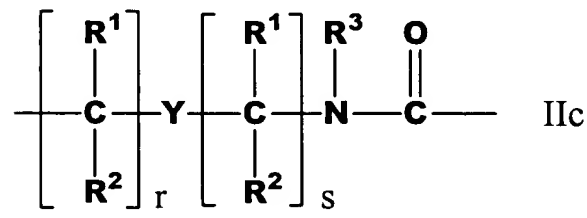
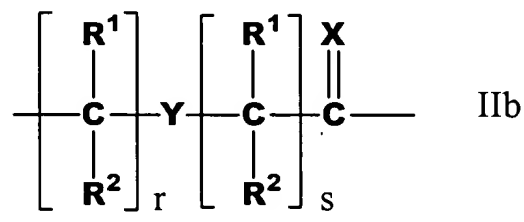
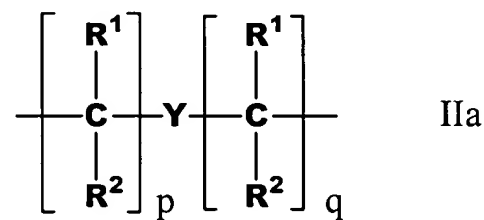
each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

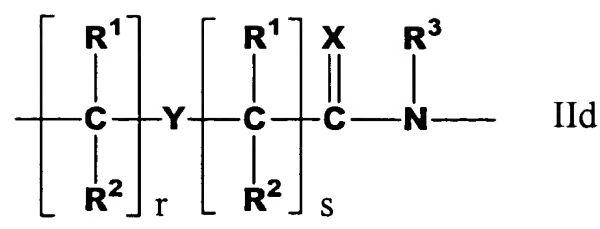
each of G<sup>1</sup>-G<sup>n-1</sup> is -NR<sup>3</sup>CO-, -NR<sup>3</sup>CS-, -NR<sup>3</sup>SO- or -NR<sup>3</sup>SO<sub>2</sub>-, in either orientation, where R<sup>3</sup> is as defined above;

each of A<sup>1</sup>-A<sup>n</sup> and B<sup>1</sup>-B<sup>n</sup> are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (IIe), and B is N or R<sup>3</sup>N<sup>+</sup>; or

(b) A is a group of formula (IIe) and B is CH;





where:

X is O, S, Se, NR<sup>3</sup>, CH<sub>2</sub> or C(CH<sub>3</sub>)<sub>2</sub>;

Y is a single bond, O, S or NR<sup>4</sup>;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R<sup>1</sup> and R<sup>2</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R<sup>3</sup> and R<sup>4</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy, alkoxy, alkylthio and amino;

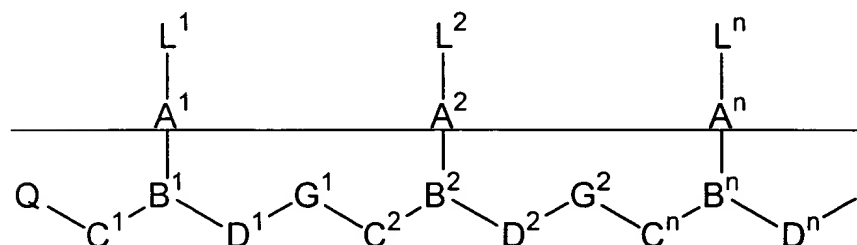
Q is -CO<sub>2</sub>H, -CONR'R'', -SO<sub>3</sub>H or -SO<sub>2</sub>NR'R'' or an activated derivative of -CO<sub>2</sub>H or -SO<sub>3</sub>H; and

I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids; and wherein:

one or more of the PNA probes of the set is suitable for detecting the presence, absence or number of human chromosome 4 in a sample wherein ~~each the probing nucleobase sequence of at least one probe comprises a probing nucleobase sequence a segment, at least a portion of which is, at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:~~

ACA-CGA-TTT-TGG-AAA-CAC (Seq. ID No. 119); CGA-AAC-ATC-ACT-GAG-AGT (Seq. ID No. 120); GGA-TGA-CAT-ATA-ATA-ACT-AG (Seq. ID

No. 121); GAA-TTG-AAC-ATT-CAC-TTT-GA (Seq. ID No. 122); TAG-CTC-TGA-AGA-TTT-CGT (Seq. ID No. 123); GAG-ATG-TTT-CCG-AGA-ATG (Seq. ID No. 124); GTG-TAT-TCA-ACT-ACC-AGA (Seq. ID No. 125); ACA-TTT-CTG-TTA-CAG-AGC (Seq. ID No. 126); ATG-ACG-TAT-AAA-ATC-TAG-AG (Seq. ID No. 127); ACG-AAC-ACA-GTT-GAA-CCT (Seq. ID No. 128) and CTC-ATA-AAA-ACC-AGA-AAG-AG (Seq. ID No. 129), wherein said PNA probes have the formula:



wherein,

$n$  is at least 2,

each of  $L^1-L^n$  is independently selected from the group consisting of hydrogen, hydroxy,  $(C_1-C_6)$ alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase binding groups, heterocyclic moieties, and reporter ligands;

each of  $C^1-C^n$  is  $(CR^6R^7)$ , where  $R^6$  is hydrogen and  $R^7$  is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or  $R^6$  and  $R^7$  are independently selected from the group consisting of hydrogen,  $(C_1-C_6)$ alkyl, aryl, aralkyl, heteroaryl, hydroxy,  $(C_1-C_6)$ alkoxy,  $(C_1-C_6)$ alkylthio,  $NR^3R^4$  and  $SR^5$ , where  $R^3$  and  $R^4$  are as defined above, and  $R^5$  is hydrogen,  $(C_1-C_6)$ alkyl, hydroxy, alkoxy, or alkylthio-substituted  $(C_1-C_6)$ alkyl, or  $R^6$  and  $R^7$  taken together complete an alicyclic or heterocyclic system;

each of  $D^1-D^n$  is  $(CR^6R^7)$ , where  $R^6$  and  $R^7$  are as defined above;

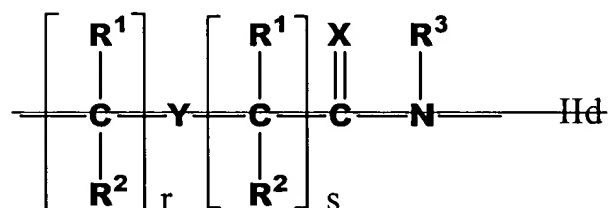
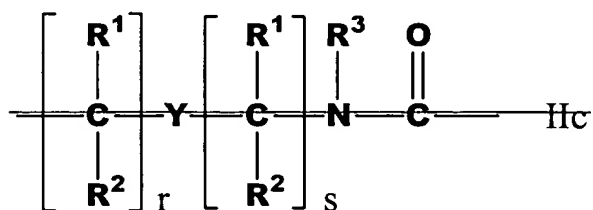
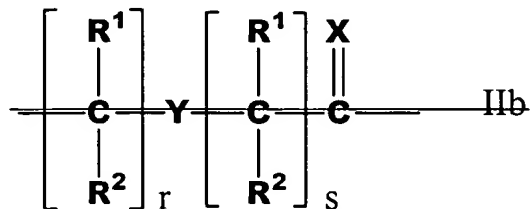
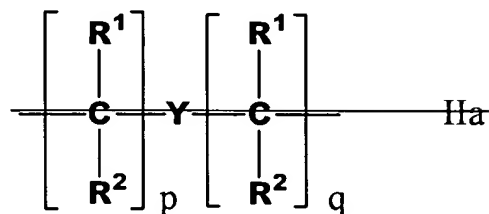
each of  $y$  and  $z$  is zero or an integer from 1 to 10, the sum  $y+z$  being greater than 2 but not more than 10;

each of  $G^1-G^n$  is  $NR^3CO$ ,  $NR^3CS$ ,  $NR^3SO$  or  $NR^3SO_2$ , in either orientation, where  $R^3$  is as defined above;

each of  $A^1-A^n$  and  $B^1-B^n$  are selected such that:

(a)  $A$  is a group of the formula (IIa), (IIb), (IIc), or (IId), and  $B$  is  $N$  or  $R^3N^+$ ; or

(b) A is a group of formula (IIa) and B is CH<sub>3</sub>;



where:

X is O, S, Se, NR<sup>3</sup>, CH<sub>3</sub> or C(CH<sub>3</sub>)<sub>2</sub>;

Y is a single bond, O, S or NR<sup>4</sup>;

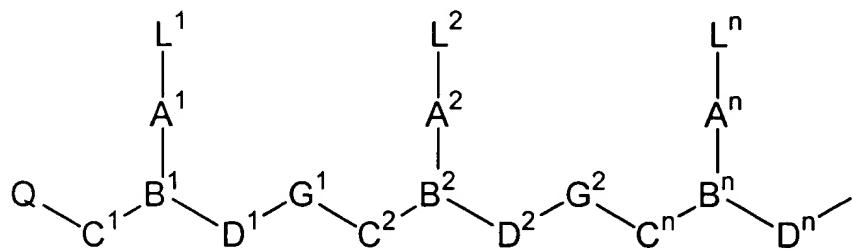
each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R<sup>1</sup> and R<sup>2</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl which may be hydroxy or alkoxy or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each  $R^3$  and  $R^4$  is independently selected from the group consisting of hydrogen,  $(C_1-C_6)$ alkyl, hydroxy or alkoxy or alkylthio substituted  $(C_1-C_6)$ alkyl, hydroxy, alkoxy, alkylthio and amino;  
 $Q$  is  $-CO_2H$ ,  $-CONR'R''$ ,  $-SO_3H$  or  $-SO_2NR'R''$  or an activated derivative of  $-CO_2H$  or  $-SO_3H$ ; and  
 $I$  is  $-NHR'''R''''$  or  $-NR'''C(O)R''''$ , where  $R'$ ,  $R''$ ,  $R'''$  and  $R''''$  are independently selected from the group consisting of hydrogen, alkyl, amino-protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids or the complement to any of the foregoing sequences.

17. (Currently Amended; Withdrawn) A probe set comprising at least one PNA probes of 10 up to 30 subunits in length wherein said PNA probe or probes have the formula:



wherein,

$n$  is at least 2,

each of  $L^1-L^n$  is independently selected from the group consisting of hydrogen, hydroxy,  $(C_1-C_6)$ alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of  $C^1-C^n$  is  $(CR^6R^7)$ , where  $R^6$  is hydrogen and  $R^7$  is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or  $R^6$  and  $R^7$  are independently selected from the group consisting of hydrogen,  $(C_1-C_6)$ alkyl, aryl, aralkyl, heteroaryl, hydroxy,  $(C_1-C_6)$ alkoxy,  $(C_1-C_6)$ alkylthio,  $NR^3R^4$  and  $SR^5$ , where  $R^3$  and  $R^4$  are as defined above, and  $R^5$  is hydrogen,  $(C_1-C_6)$ alkyl, hydroxy-, alkoxy-, or alkylthio-

substituted (C<sub>1</sub>-C<sub>6</sub>)alkyl, or R<sup>6</sup> and R<sup>7</sup> taken together complete an alicyclic or heterocyclic system;

each of D<sup>1</sup>-D<sup>n</sup> is (CR<sup>6</sup>R<sup>7</sup>), where R<sup>6</sup> and R<sup>7</sup> are as defined above;

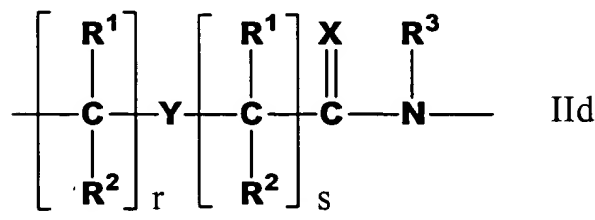
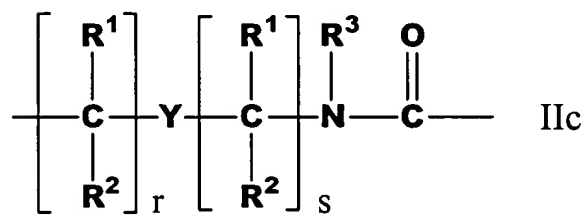
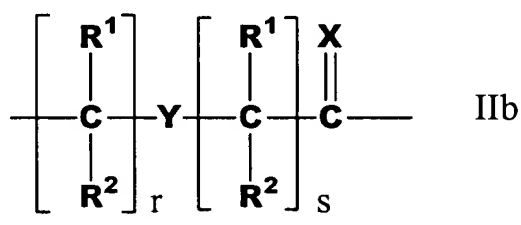
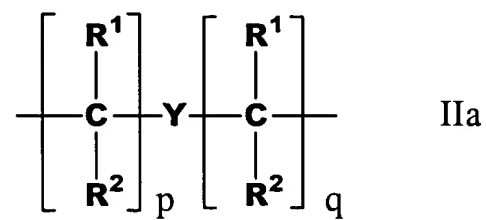
each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

each of G<sup>1</sup>-G<sup>n-1</sup> is -NR<sup>3</sup>CO-, -NR<sup>3</sup>CS-, -NR<sup>3</sup>SO- or -NR<sup>3</sup>SO<sub>2</sub>-, in either orientation, where R<sup>3</sup> is as defined above;

each of A<sup>1</sup>-A<sup>n</sup> and B<sup>1</sup>-B<sup>n</sup> are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (IIId), and B is N or R<sup>3</sup>N<sup>+</sup>; or

(b) A is a group of formula (IIId) and B is CH;



where:

X is O, S, Se, NR<sup>3</sup>, CH<sub>2</sub> or C(CH<sub>3</sub>)<sub>2</sub>;

Y is a single bond, O, S or NR<sup>4</sup>;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R<sup>1</sup> and R<sup>2</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R<sup>3</sup> and R<sup>4</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy, alkoxy, alkylthio and amino;

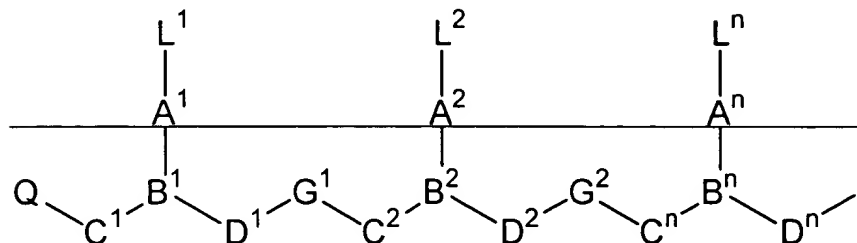
Q is -CO<sub>2</sub>H, -CONR'R'', -SO<sub>3</sub>H or -SO<sub>2</sub>NR'R'' or an activated derivative of -CO<sub>2</sub>H or -SO<sub>3</sub>H; and

I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids; and wherein:

one or more of the PNA probes of the set is suitable for detecting the presence, absence or number of human chromosome 7 in a sample wherein ~~each the probing nucleobase sequence of at least one probe comprises a probing nucleobase sequence segment, at least a portion of which is, at least ninety percent homologous to the nucleobase sequences, or their complements,~~ selected from the group consisting of:

CAG-TTC-ATA-TGT-GCA-GTG (Seq. ID No. 130); GGA-ATA-TCG-TCA-CCT-AAA (Seq. ID No. 131); TGG-AGC-AAA-TTG-AAG-CCT (Seq. ID No. 132); TGG-AGC-ACA-TTT-ATG-CCT (Seq. ID No. 133); TGC-ATT-CTA-CTC-CCA-TAG (Seq. ID No. 134); ACA-CTC-TGT-TTC-TAA-AAT-CT (Seq. ID No. 135); GCA-GGC-GGA-TAT-TTA-GTA (Seq. ID No. 136); AGC-GAT-TTG-ATG-CCA-ACA (Seq. ID No. 137); TTG-CAA-ACG-GGG-TTT-CTT (Seq. ID No. 138); CTT-TCA-TGC-TAG-ACA-GAA (Seq. ID No. 139); CAA-AAA-AGT-TAC-TGA-GAA-C (Seq. ID No. 140); AAA-ATG-CCA-CAG-CAA-GAG (Seq. ID No. 141); GTT-TGA-AAA-CAC-ACT-GTT-TG

(Seq. ID No. 142); ATA-TGG-ACC-TGT-TTG-AGG (Seq. ID No. 143); and CAT-TGA-ATG-CTA-GAC-GGA (Seq. ID No. 144), wherein said PNA probes have the formula:



wherein,

$n$  is at least 2;

each of  $L^1$ - $L^n$  is independently selected from the group consisting of hydrogen, hydroxy,  $(C_1-C_6)$ alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of  $C^1$ - $C^n$  is  $(CR^6R^7)_x$ , where  $R^6$  is hydrogen and  $R^7$  is selected from the group consisting of the side chains of naturally occurring alpha-amino acids, or  $R^6$  and  $R^7$  are independently selected from the group consisting of hydrogen,  $(C_1-C_6)$ alkyl, aryl, aralkyl, heteroaryl, hydroxy,  $(C_1-C_6)$ alkoxy,  $(C_1-C_6)$ alkylthio,  $NR^3R^4$  and  $SR^5$ , where  $R^3$  and  $R^4$  are as defined above, and  $R^5$  is hydrogen,  $(C_1-C_6)$ alkyl, hydroxy, alkoxy, or alkylthio-substituted  $(C_1-C_6)$ alkyl, or  $R^6$  and  $R^7$  taken together complete an alicyclic or heterocyclic system;

each of  $D^1$ - $D^n$  is  $(CR^6R^7)_z$ , where  $R^6$  and  $R^7$  are as defined above;

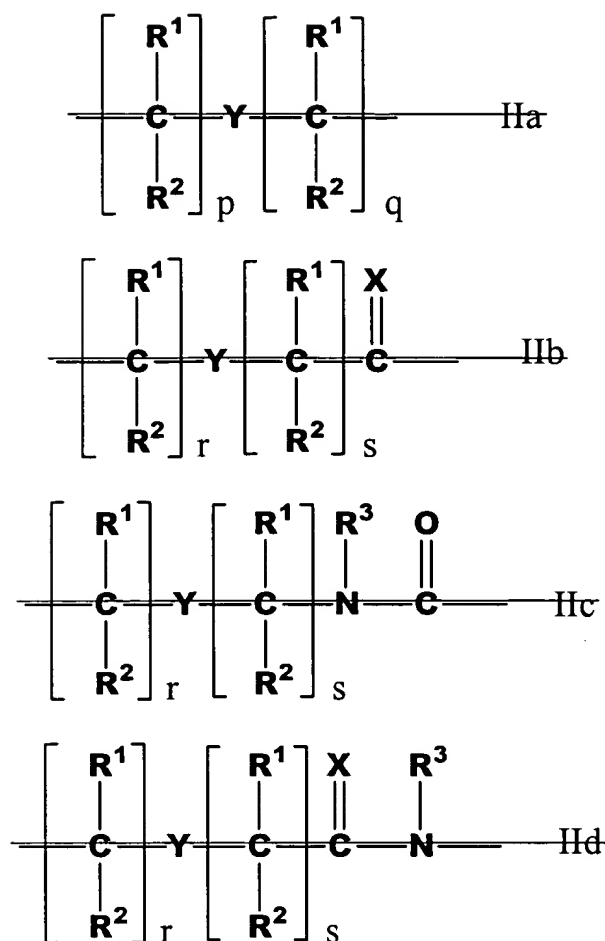
each of  $y$  and  $z$  is zero or an integer from 1 to 10, the sum  $y+z$  being greater than 2 but not more than 10;

each of  $G^1$ - $G^n$  is  $NR^3CO$ ,  $NR^3CS$ ,  $NR^3SO$  or  $NR^3SO_2$ , in either orientation, where  $R^3$  is as defined above;

each of  $A^1$ - $A^n$  and  $B^1$ - $B^n$  are selected such that:

- (a)  $A$  is a group of the formula (IIa), (IIb), (IIc), or (IIe), and  $B$  is  $N$  or  $R^3N$ ; or
- (b)  $A$  is a group of formula (IIe) and  $B$  is  $CH$ ;





where:

X is O, S, Se, NR<sup>3</sup>, CH<sub>2</sub> or C(CH<sub>3</sub>)<sub>2</sub>;

Y is a single bond, O, S or NR<sup>4</sup>;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

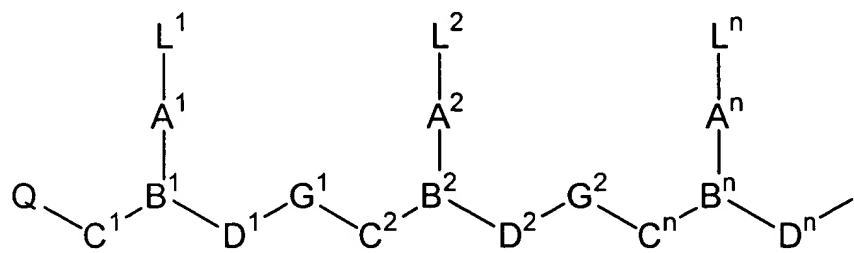
each R<sup>1</sup> and R<sup>2</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl which may be hydroxy or alkoxy or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R<sup>3</sup> and R<sup>4</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy or alkoxy or alkylthio-substituted (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is  $\text{CO}_2\text{H}$ ,  $\text{CONR}'\text{R}''$ ,  $\text{SO}_3\text{H}$  or  $\text{SO}_2\text{NR}'\text{R}''$  or an activated derivative of  $\text{CO}_2\text{H}$  or  $\text{SO}_3\text{H}$ ; and

I is  $\text{NHR}'''\text{R}''''$  or  $\text{NR}'''\text{C}(\text{O})\text{R}''''$ , where  $\text{R}'$ ,  $\text{R}''$ ,  $\text{R}'''$  and  $\text{R}''''$  are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids or the complement to any of the foregoing sequences.

18. (Currently Amended; Withdrawn) A probe set comprising at least one PNA probes of ~~10~~ up to 30 subunits in length wherein said PNA probe or probes have the formula:



wherein,

n is at least 2,

each of  $\text{L}^1$ - $\text{L}^n$  is independently selected from the group consisting of hydrogen, hydroxy,  $(\text{C}_1\text{-C}_4)$ alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of  $\text{C}^1$ - $\text{C}^n$  is  $(\text{CR}^6\text{R}^7)$ , where  $\text{R}^6$  is hydrogen and  $\text{R}^7$  is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or  $\text{R}^6$  and  $\text{R}^7$  are independently selected from the group consisting of hydrogen,  $(\text{C}_2\text{-C}_6)$ alkyl, aryl, aralkyl, heteroaryl, hydroxy,  $(\text{C}_1\text{-C}_6)$ alkoxy,  $(\text{C}_1\text{-C}_6)$ alkylthio,  $\text{NR}^3\text{R}^4$  and  $\text{SR}^5$ , where  $\text{R}^3$  and  $\text{R}^4$  are as defined above, and  $\text{R}^5$  is hydrogen,  $(\text{C}_1\text{-C}_6)$ alkyl, hydroxy-, alkoxy-, or alkylthio-substituted  $(\text{C}_1\text{-C}_6)$ alkyl, or  $\text{R}^6$  and  $\text{R}^7$  taken together complete an alicyclic or heterocyclic system;

each of  $\text{D}^1$ - $\text{D}^n$  is  $(\text{CR}^6\text{R}^7)$ , where  $\text{R}^6$  and  $\text{R}^7$  are as defined above;

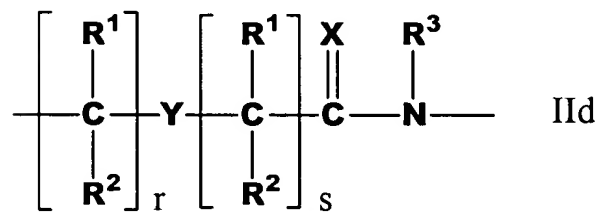
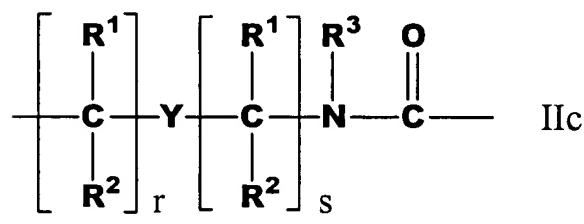
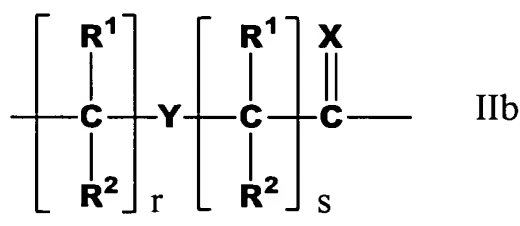
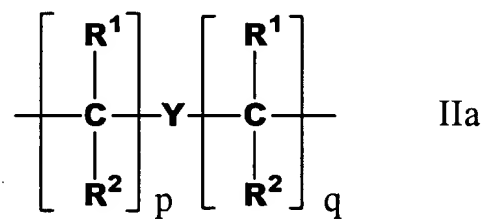
each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

each of  $G^1$ - $G^{n-1}$  is  $-\text{NR}^3\text{CO}-$ ,  $-\text{NR}^3\text{CS}-$ ,  $-\text{NR}^3\text{SO}-$  or  $-\text{NR}^3\text{SO}_2-$ , in either orientation, where  $\text{R}^3$  is as defined above;

each of  $\text{A}^1$ - $\text{A}^n$  and  $\text{B}^1$ - $\text{B}^n$  are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (II d), and B is N or  $\text{R}^3\text{N}^+$ ; or

(b) A is a group of formula (II d) and B is  $\text{CH}$ ;



where:

X is O, S, Se,  $\text{NR}^3$ ,  $\text{CH}_2$  or  $\text{C}(\text{CH}_3)_2$ ;

Y is a single bond, O, S or  $\text{NR}^4$ ;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

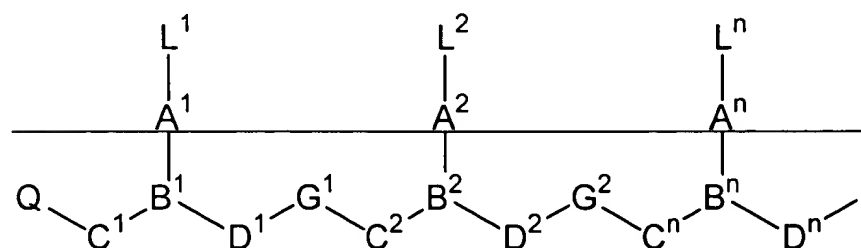
each R<sup>1</sup> and R<sup>2</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R<sup>3</sup> and R<sup>4</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is -CO<sub>2</sub>H, -CONR'R'', -SO<sub>3</sub>H or -SO<sub>2</sub>NR'R'' or an activated derivative of -CO<sub>2</sub>H or -SO<sub>3</sub>H; and

I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids; and wherein:

one or more of the PNA probes of the set is suitable for detecting the presence, absence or number of human chromosome 9 in a sample wherein ~~each the probing nucleobase sequence of at least one~~ probe comprises a probing nucleobase sequence segment, at least a portion of which is, at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of: ATG-ATG-AAA-AAG-GTA-ATA (Seq. ID No. 145) and CAT-TCT-CAG-AAC-TGT-TTG (Seq. ID No. 146), wherein said PNA probes have the formula:



wherein,

~~n is at least 2;~~

~~each of L<sup>1</sup>-L<sup>n</sup> is independently selected from the group consisting of hydrogen, hydroxy, (C<sub>1</sub>-C<sub>4</sub>)alkanoyl, naturally occurring nucleobases, aromatic moieties,~~

DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of  $E^1-E^n$  is  $(CR^6R^7)_p$ , where  $R^6$  is hydrogen and  $R^7$  is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or  $R^6$  and  $R^7$  are independently selected from the group consisting of hydrogen,  $(C_2-C_6)$ alkyl, aryl, aralkyl, heteroaryl, hydroxy,  $(C_2-C_6)$ alkoxy,  $(C_2-C_6)$ alkylthio,  $NR^3R^4$  and  $SR^5$ , where  $R^3$  and  $R^4$  are as defined above, and  $R^5$  is hydrogen,  $(C_2-C_6)$ alkyl, hydroxy, alkoxy, or alkylthio-substituted  $(C_2-C_6)$ alkyl, or  $R^6$  and  $R^7$  taken together complete an alicyclic or heterocyclic system;

each of  $D^1-D^z$  is  $(CR^6R^7)_z$ , where  $R^6$  and  $R^7$  are as defined above;

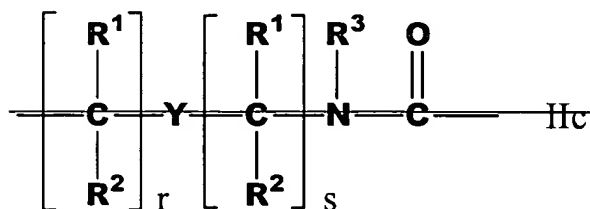
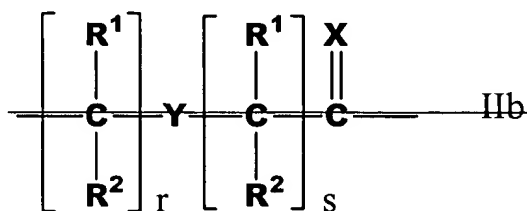
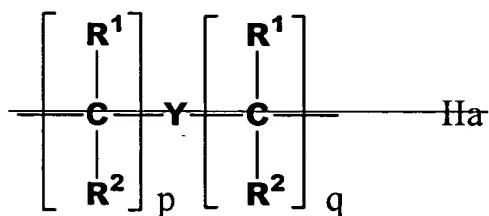
each of  $y$  and  $z$  is zero or an integer from 1 to 10, the sum  $y+z$  being greater than 2 but not more than 10;

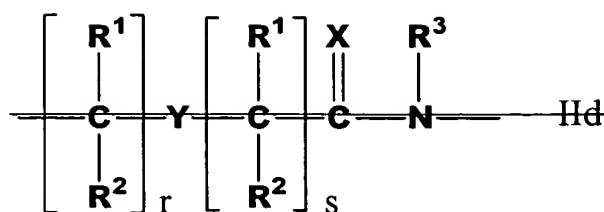
each of  $G^1-G^{n+1}$  is  $NR^3CO$ ,  $NR^3CS$ ,  $NR^3SO$  or  $NR^3SO_2$ , in either orientation, where  $R^3$  is as defined above;

each of  $A^1-A^n$  and  $B^1-B^n$  are selected such that:

(a)  $A$  is a group of the formula (IIa), (IIb), (IIc), or (IId), and  $B$  is  $N$  or  $R^3N^+$ ; or

(b)  $A$  is a group of formula (IId) and  $B$  is  $CH_2$ ;





where:

X is O, S, Se, NR<sup>3</sup>, CH<sub>2</sub> or C(CH<sub>3</sub>)<sub>2</sub>;

Y is a single bond, O, S or NR<sup>4</sup>;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

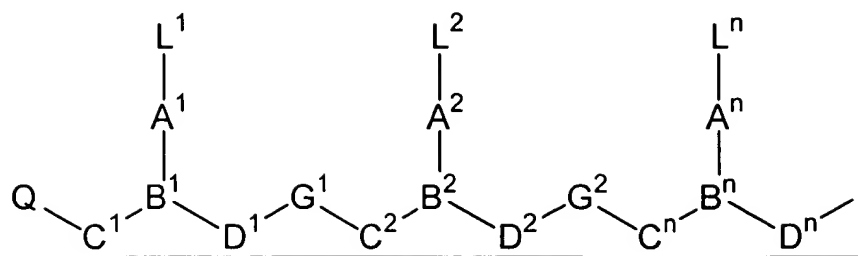
each R<sup>1</sup> and R<sup>2</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl which may be hydroxy or alkoxy or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R<sup>3</sup> and R<sup>4</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy or alkoxy or alkylthio-substituted (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is CO<sub>2</sub>H, CONR'R'', SO<sub>3</sub>H or SO<sub>2</sub>NR'R'' or an activated derivative of CO<sub>2</sub>H or SO<sub>3</sub>H; and

H is NHR'''R'''' or NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids or the complement to any of the foregoing sequences.

19. (Currently Amended; Withdrawn) A probe set comprising at least one PNA probes of 10 up to 30 subunits in length wherein said PNA probe or probes have the formula:



wherein,

n is at least 2,

each of  $L^1$ - $L^n$  is independently selected from the group consisting of hydrogen, hydroxy,  $(C_1-C_4)$ alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of  $C^1$ - $C^n$  is  $(CR^6R^7)$ , where  $R^6$  is hydrogen and  $R^7$  is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or  $R^6$  and  $R^7$  are independently selected from the group consisting of hydrogen,  $(C_1-C_6)$ alkyl, aryl, aralkyl, heteroaryl, hydroxy,  $(C_1-C_6)$ alkoxy,  $(C_1-C_6)$ alkylthio,  $NR^3R^4$  and  $SR^5$ , where  $R^3$  and  $R^4$  are as defined above, and  $R^5$  is hydrogen,  $(C_1-C_6)$ alkyl, hydroxy-, alkoxy-, or alkylthio-substituted  $(C_1-C_6)$ alkyl, or  $R^6$  and  $R^7$  taken together complete an alicyclic or heterocyclic system;

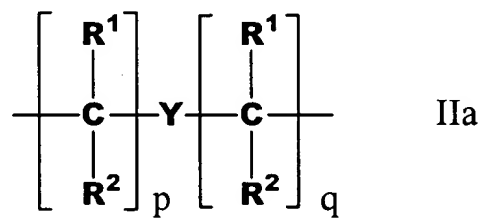
each of  $D^1$ - $D^n$  is  $(CR^6R^7)$ , where  $R^6$  and  $R^7$  are as defined above;

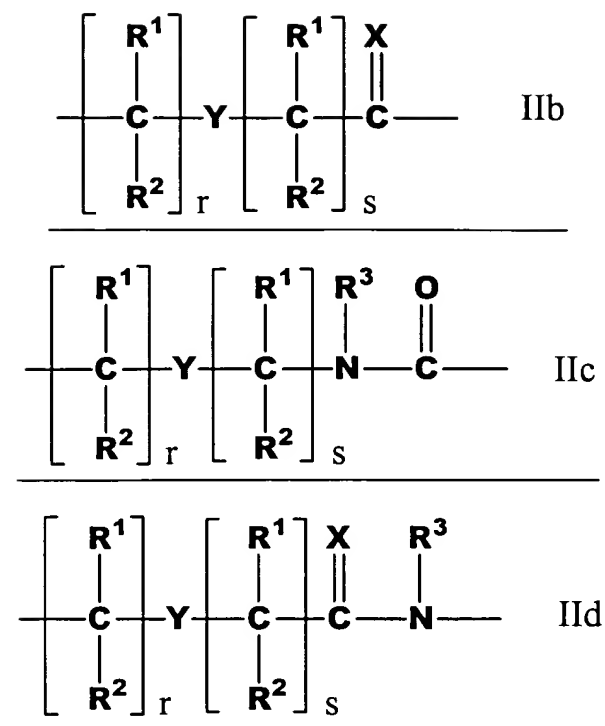
each of y and z is zero or an integer from 1 to 10, the sum  $y+z$  being greater than 2 but not more than 10;

each of  $G^1$ - $G^{n-1}$  is  $-NR^3CO-$ ,  $-NR^3CS-$ ,  $-NR^3SO-$  or  $-NR^3SO_2-$ , in either orientation, where  $R^3$  is as defined above;

each of  $A^1$ - $A^n$  and  $B^1$ - $B^n$  are selected such that:

- (a) A is a group of the formula (IIa), (IIb), (IIc), or (IId), and B is N or  $R^3N^+$ ; or  
(b) A is a group of formula (IId) and B is CH;





where:

X is O, S, Se, NR<sup>3</sup>, CH<sub>2</sub> or C(CH<sub>3</sub>)<sub>2</sub>;

Y is a single bond, O, S or NR<sup>4</sup>;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R<sup>1</sup> and R<sup>2</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

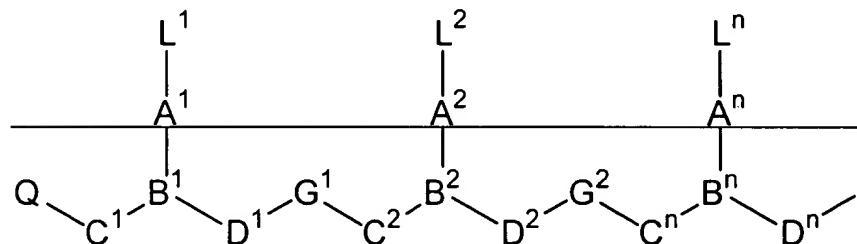
each R<sup>3</sup> and R<sup>4</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is -CO<sub>2</sub>H, -CONR'R'', -SO<sub>3</sub>H or -SO<sub>2</sub>NR'R'' or an activated derivative of -CO<sub>2</sub>H or -SO<sub>3</sub>H; and

L is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl,



amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids; and wherein: one or more of the PNA probes of the set is suitable for detecting the presence, absence or number of human chromosome 20 in a sample wherein each the probing nucleobase sequence of at least one probe comprises a probing nucleobase sequence segment, at least a portion of which is, at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of: ACA-GAA-CTA-AAC-CAT-CGT (Seq. ID No. 147); TAG-GCC-AGC-TTG-GAG-GAT (Seq. ID No. 148); CTA-GCT-GGG-AGG-ATT-T (Seq. ID No. 149); TGT-GCC-TCA-ACT-GAC-A (Seq. ID No. 150); TGC-TTT-GGG-ATG-TTT-CAA (Seq. ID No. 151); and GCA-ATG-TCA-GAA-CTT-TTT-TC (Seq. ID No. 152), wherein said PNA probes have the formula:



wherein,

$n$  is at least 2,

each of  $L^1-L^n$  is independently selected from the group consisting of hydrogen, hydroxy,  $(C_1-C_6)$ alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase binding groups, heterocyclic moieties, and reporter ligands;

each of  $C^1-C^n$  is  $(CR^6R^7)$ , where  $R^6$  is hydrogen and  $R^7$  is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or  $R^6$  and  $R^7$  are independently selected from the group consisting of hydrogen,  $(C_1-C_6)$ alkyl, aryl, aralkyl, heteroaryl, hydroxy,  $(C_1-C_6)$ alkoxy,  $(C_1-C_6)$ alkylthio,  $NR^3R^4$  and  $SR^5$ , where  $R^3$  and  $R^4$  are as defined above, and  $R^5$  is hydrogen,  $(C_1-C_6)$ alkyl, hydroxy, alkoxy, or alkylthio substituted  $(C_1-C_6)$ alkyl, or  $R^6$  and  $R^7$  taken together complete an alicyclic or heterocyclic system;

each of  $D^1-D^n$  is  $(CR^6R^7)$ , where  $R^6$  and  $R^7$  are as defined above;

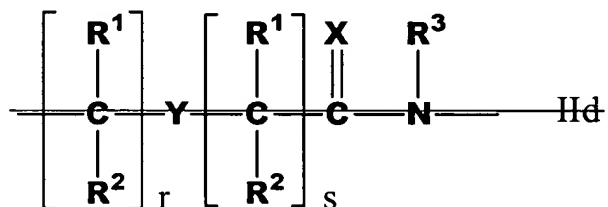
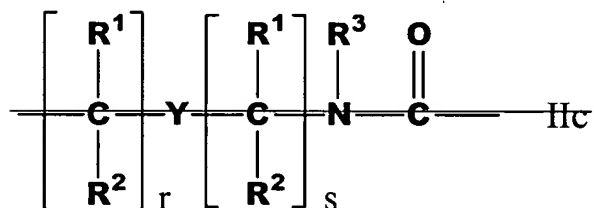
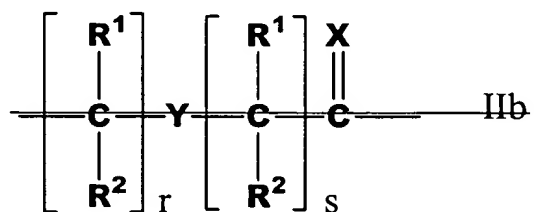
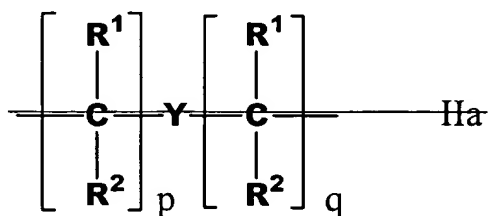
each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

each of  $G^1-G^{n+1}$  is  $\text{NR}^3\text{CO}$ ,  $\text{NR}^3\text{CS}$ ,  $\text{NR}^3\text{SO}$  or  $\text{NR}^3\text{SO}_2$ , in either orientation, where  $\text{R}^3$  is as defined above;

each of  $\text{A}^1-\text{A}^n$  and  $\text{B}^1-\text{B}^n$  are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (II d), and B is N or  $\text{R}^3\text{N}$ ; or

(b) A is a group of formula (II d) and B is  $\text{CH}$ ;



where:

X is O, S, Se,  $\text{NR}^3$ ,  $\text{CH}_2$  or  $\text{C}(\text{CH}_3)_2$ ;

Y is a single bond, O, S or  $\text{NR}^4$ ;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

~~each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;~~

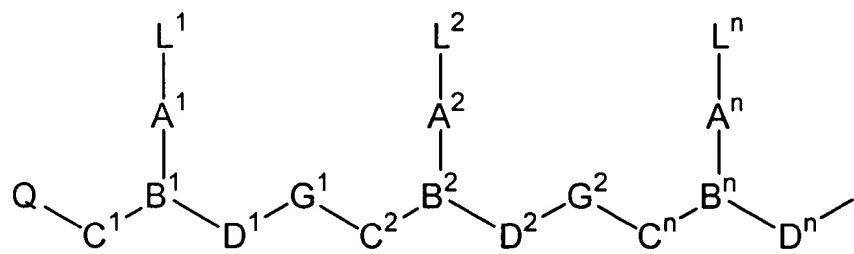
~~each R<sup>1</sup> and R<sup>2</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl which may be hydroxy or alkoxy or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and~~

~~each R<sup>3</sup> and R<sup>4</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy or alkoxy or alkylthio-substituted (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy, alkoxy, alkylthio and amino;~~

~~Q is -CO<sub>2</sub>H, -CONR'R'', -SO<sub>3</sub>H or -SO<sub>2</sub>NR'R'' or an activated derivative of -CO<sub>2</sub>H or -SO<sub>3</sub>H; and~~

~~I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids or the complement to any of the foregoing sequences.~~

20. (Currently Amended; Withdrawn) A probe set comprising at least one PNA probes of ~~10~~ up to 30 subunits in length wherein said PNA probe or probes have the formula:



wherein,

n is at least 2,

each of L<sup>1</sup>-L<sup>n</sup> is independently selected from the group consisting of hydrogen, hydroxy, (C<sub>1</sub>-C<sub>4</sub>)alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C<sup>1</sup>-C<sup>n</sup> is (CR<sup>6</sup>R<sup>7</sup>)<sub>y</sub>, where R<sup>6</sup> is hydrogen and R<sup>7</sup> is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R<sup>6</sup> and R<sup>7</sup> are independently selected from the group consisting of hydrogen, (C<sub>2</sub>-C<sub>6</sub>)alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C<sub>1</sub>-C<sub>6</sub>)alkoxy, (C<sub>1</sub>-C<sub>6</sub>)alkylthio, NR<sup>3</sup>R<sup>4</sup> and SR<sup>5</sup>, where R<sup>3</sup> and R<sup>4</sup> are as defined above, and R<sup>5</sup> is hydrogen, (C<sub>1</sub>-C<sub>6</sub>)alkyl, hydroxy-, alkoxy-, or alkylthio-substituted (C<sub>1</sub>-C<sub>6</sub>)alkyl, or R<sup>6</sup> and R<sup>7</sup> taken together complete an alicyclic or heterocyclic system;

each of D<sup>1</sup>-D<sup>n</sup> is (CR<sup>6</sup>R<sup>7</sup>)<sub>z</sub>, where R<sup>6</sup> and R<sup>7</sup> are as defined above;

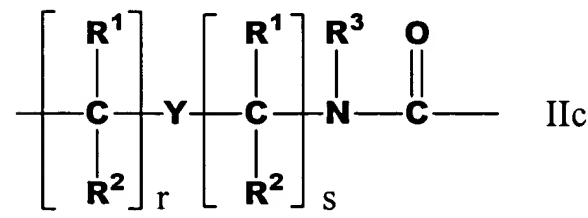
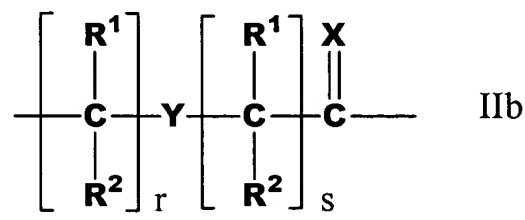
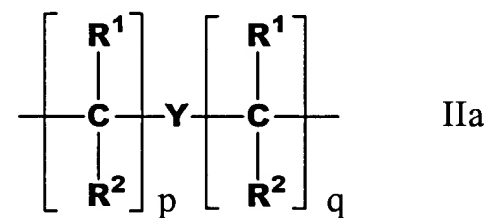
each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

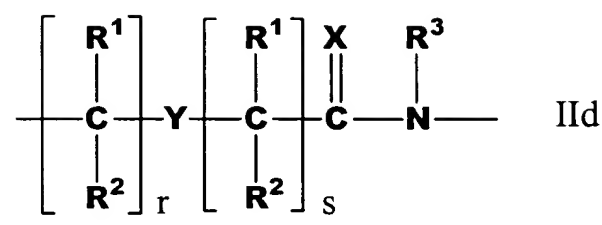
each of G<sup>1</sup>-G<sup>n-1</sup> is -NR<sup>3</sup>CO-, -NR<sup>3</sup>CS-, -NR<sup>3</sup>SO- or -NR<sup>3</sup>SO<sub>2</sub>-, in either orientation, where R<sup>3</sup> is as defined above;

each of A<sup>1</sup>-A<sup>n</sup> and B<sup>1</sup>-B<sup>n</sup> are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (IIId), and B is N or R<sup>3</sup>N<sup>+</sup>; or

(b) A is a group of formula (IIId) and B is CH;





where:

X is O, S, Se, NR<sup>3</sup>, CH<sub>2</sub> or C(CH<sub>3</sub>)<sub>2</sub>;

Y is a single bond, O, S or NR<sup>4</sup>;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R<sup>1</sup> and R<sup>2</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R<sup>3</sup> and R<sup>4</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy, alkoxy, alkylthio and amino;

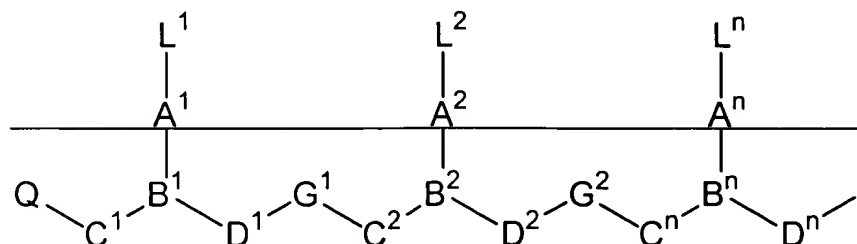
Q is -CO<sub>2</sub>H, -CONR'R'', -SO<sub>3</sub>H or -SO<sub>2</sub>NR'R'' or an activated derivative of -CO<sub>2</sub>H or -SO<sub>3</sub>H; and

I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids; and wherein:

one or more of the PNA probes of the set is suitable for detecting the presence, absence or number of human chromosomes 13 and 21 as a pair in a sample wherein each the ~~probing nucleobase sequence of at least one~~ probe comprises a probing nucleobase sequence segment, ~~at least a portion of which is, at least ninety percent homologous to the nucleobase sequences, or their complements,~~ selected from the group consisting of: CCG-AAA-GAA-ATT-TGT-GGG (Seq. ID No. 153); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 154); TCA-AGG-CGA-TCG-AAA-TGT (Seq. ID No.

155); GAG-ACA-CAT-ATC-ACC-AAC (Seq. ID No. 156); CAG-AAA-TTT-CTT-TCG-GAT-A (Seq. ID No. 157); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 158) and AGC-CAA-AGG-AGT-TGA-ACA (Seq. ID No. 159),

wherein said PNA probes have the formula:



wherein;

n is at least 2;

each of  $L^1$ - $L^n$  is independently selected from the group consisting of hydrogen, hydroxy,  $(C_1-C_6)$ alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase binding groups, heterocyclic moieties, and reporter ligands;

each of  $C^1$ - $C^n$  is  $(CR^6R^7)$ , where  $R^6$  is hydrogen and  $R^7$  is selected from the group consisting of the side chains of naturally occurring alpha-amino acids, or  $R^6$  and  $R^7$  are independently selected from the group consisting of hydrogen,  $(C_2-C_6)$ alkyl, aryl, aralkyl, heteroaryl, hydroxy,  $(C_1-C_6)$ alkoxy,  $(C_1-C_6)$ alkylthio,  $NR^3R^4$  and  $SR^5$ , where  $R^3$  and  $R^4$  are as defined above, and  $R^5$  is hydrogen,  $(C_1-C_6)$ alkyl, hydroxy, alkoxy, or alkylthio-substituted  $(C_1-C_6)$ alkyl, or  $R^6$  and  $R^7$  taken together complete an alicyclic or heterocyclic system;

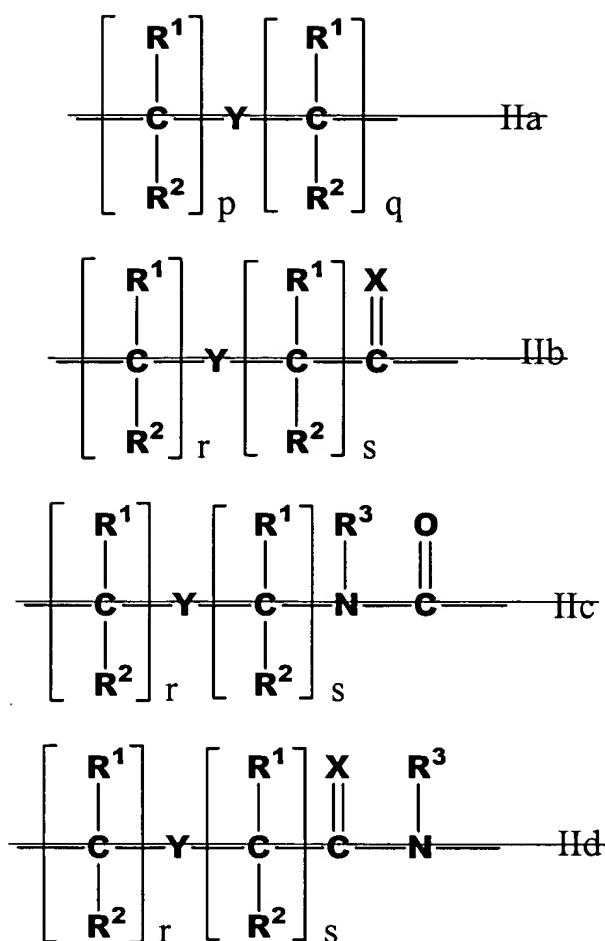
each of  $D^1$ - $D^n$  is  $(CR^6R^7)$ , where  $R^6$  and  $R^7$  are as defined above;

each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

each of  $G^1$ - $G^{n+1}$  is  $NR^3CO$ ,  $NR^3CS$ ,  $NR^3SO$  or  $NR^3SO_2$ , in either orientation, where  $R^3$  is as defined above;

each of  $A^1$ - $A^n$  and  $B^1$ - $B^n$  are selected such that:

- (a) A is a group of the formula (IIa), (IIb), (IIc), or (IIe), and B is N or  $R^3N^+$ ; or
- (b) A is a group of formula (IIe) and B is  $CH$ ;



where:

X is O, S, Se, NR<sup>3</sup>, CH<sub>2</sub> or C(CH<sub>3</sub>)<sub>2</sub>;

Y is a single bond, O, S or NR<sup>4</sup>;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R<sup>1</sup> and R<sup>2</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl which may be hydroxy or alkoxy or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

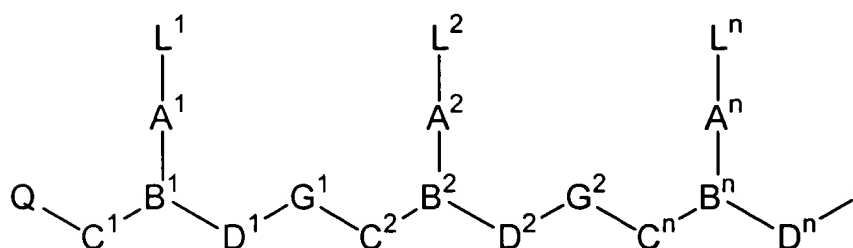
each R<sup>3</sup> and R<sup>4</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy or alkoxy or alkylthio-substituted (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy, alkoxy, alkylthio and amino;

~~Q is  $\text{CO}_2\text{H}$ ,  $\text{CONR}'\text{R}''$ ,  $\text{SO}_3\text{H}$  or  $\text{SO}_2\text{NR}'\text{R}''$  or an activated derivative of  $\text{CO}_2\text{H}$  or  $\text{SO}_3\text{H}$ ; and~~

~~L is  $\text{NHR}'''\text{R}''''$  or  $\text{NR}'''\text{C}(\text{O})\text{R}''''$ , where  $\text{R}'$ ,  $\text{R}''$ ,  $\text{R}'''$  and  $\text{R}''''$  are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids or the complement to any of the foregoing sequences.~~

21. (Currently Amended) A method comprising:

- a) contacting ~~the a~~ sample with one or more PNA probes of up to 30 subunits in length comprising a probing nucleobase sequence wherein each probe is specific for one or more of human chromosomes Y, 1, 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 16, 17, 18 or 20, as well as 13/21 as a pair; and
- b) detecting, identify or quantitating hybridization of the probing nucleobase sequence of the PNA probe or probes to the target sequences of the chromosomes, and correlating the result with the presence, absence or number of the chromosomes in the sample; wherein said PNA probes have the formula:



wherein,

n is at least 2,

each of  $\text{L}^1\text{-L}^n$  is independently selected from the group consisting of hydrogen, hydroxy,  $(\text{C}_1\text{-C}_4)$ alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of  $\text{C}^1\text{-C}^n$  is  $(\text{CR}^6\text{R}^7)$ , where  $\text{R}^6$  is hydrogen and  $\text{R}^7$  is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or  $\text{R}^6$  and  $\text{R}^7$  are independently selected from the group consisting of hydrogen,



(C<sub>2</sub>-C<sub>6</sub>)alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C<sub>1</sub>-C<sub>6</sub>)alkoxy, (C<sub>1</sub>-C<sub>6</sub>)alkylthio, NR<sup>3</sup>R<sup>4</sup> and SR<sup>5</sup>, where R<sup>3</sup> and R<sup>4</sup> are as defined above, and R<sup>5</sup> is hydrogen, (C<sub>1</sub>-C<sub>6</sub>)alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C<sub>1</sub>-C<sub>6</sub>)alkyl, or R<sup>6</sup> and R<sup>7</sup> taken together complete an alicyclic or heterocyclic system;

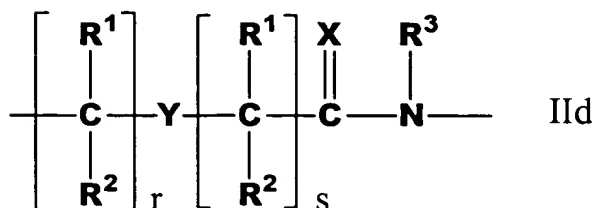
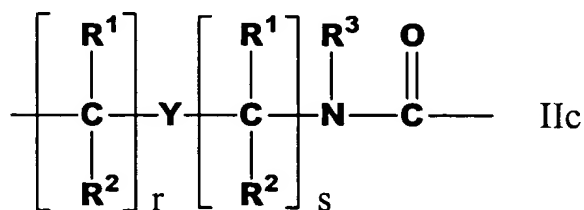
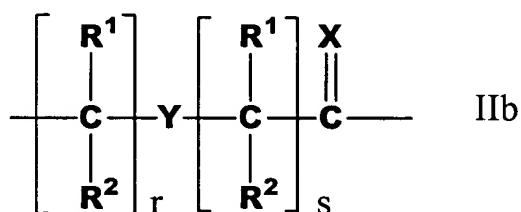
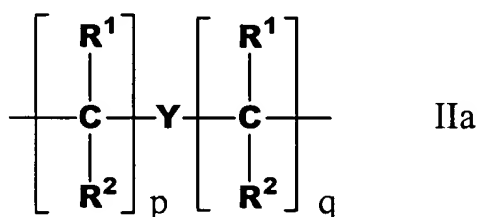
each of D<sup>1</sup>-D<sup>n</sup> is (CR<sup>6</sup>R<sup>7</sup>)<sub>z</sub> where R<sup>6</sup> and R<sup>7</sup> are as defined above;

each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

each of G<sup>1</sup>-G<sup>n-1</sup> is -NR<sup>3</sup>CO-, -NR<sup>3</sup>CS-, -NR<sup>3</sup>SO- or -NR<sup>3</sup>SO<sub>2</sub>-, in either orientation, where R<sup>3</sup> is as defined above;

each of A<sup>1</sup>-A<sup>n</sup> and B<sup>1</sup>-B<sup>n</sup> are selected such that:

- (a) A is a group of the formula (IIa), (IIb), (IIc), or (IId), and B is N or R<sup>3</sup>N'; or
- (b) A is a group of formula (IId) and B is CH;



where:

X is O, S, Se,  $\text{NR}^3$ ,  $\text{CH}_2$  or  $\text{C}(\text{CH}_3)_2$ ;

Y is a single bond, O, S or  $\text{NR}^4$ ;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each  $\text{R}^1$  and  $\text{R}^2$  is independently selected from the group consisting of hydrogen,  $(\text{C}_1\text{-C}_4)$ alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each  $\text{R}^3$  and  $\text{R}^4$  is independently selected from the group consisting of hydrogen,  $(\text{C}_1\text{-C}_4)$ alkyl, hydroxy- or alkoxy- or alkylthio-substituted  $(\text{C}_1\text{-C}_4)$ alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is  $-\text{CO}_2\text{H}$ ,  $-\text{CONR}'\text{R}''$ ,  $-\text{SO}_3\text{H}$  or  $-\text{SO}_2\text{NR}'\text{R}''$  or an activated derivative of  $-\text{CO}_2\text{H}$  or  $-\text{SO}_3\text{H}$ ; and

I is  $-\text{NHR}'''\text{R}''''$  or  $-\text{NR}'''\text{C}(\text{O})\text{R}''''$ , where  $\text{R}'$ ,  $\text{R}''$ ,  $\text{R}'''$  and  $\text{R}''''$  are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids and wherein;  
the probing nucleobase sequence of the at least one probe comprises  
a probing nucleobase sequence selected from the group consisting  
of:

CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT (Seq. ID No. 15); GGC-ATA-GCA-CAT-AAC-ATG (Seq. ID No. 16); AAT-CGT-CAT-CGA-ATG-AAT (Seq. ID No. 17); CAT-TGA-ACA-GAA-TTG-AAT (Seq. ID No. 18); GTT-TTC-AGG-GGA-AGA-TAT (Seq. ID No. 19); TGT-GCG-CCC-TCA-ACT-AAC (Seq. ID No. 20); GAA-GCT-TCA-TTG-GGA-TGT (Seq. ID No. 21); CCA-ATA-AAA-GCT-ACA-TAG-A (Seq. ID No. 22); GAA-AAA-GTT-TCT-GAC-ATT-GC

(Seq. ID No. 23); TAG-TTG-AAG-GGC-ACA-TCA (Seq. ID No. 24); CAC-AAA-TAA-GAT-TCT-AAG-AAT (Seq. ID No. 25); TCA-AAA-GAA-TGC-TTC-AAC-AC (Seq. ID No. 26); ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27); GCT-GTT-TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-AGG-TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID No. 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-TCA-ACT-CAC-GGA (Seq. ID No. 32); CCT-CAC-AAA-GTA-GAA-ACT (Seq. ID No. 33); GAA-AAA-GCA-GTT-ACT-GAG (Seq. ID No. 34); TAA-TAA-TTA-GAC-GGA-ATC-AT (Seq. ID No. 35); TTA-CAG-GGC-ATT-GAA-GCC (Seq. ID No. 36); CAG-TTA-TGA-AGC-AGT-CTC (Seq. ID No. 37); CAC-ACC-AGA-AAA-AGC-AGT (Seq. ID No. 38); AAG-GGT-AAA-CAC-TGT-GAG (Seq. ID No. 39); AGA-CAA-CGA-AAT-ATC-TTC-ATG (Seq. ID No. 40); CTA-GCA-GTA-TGA-GGT-CAA (Seq. ID No. 41); GCA-GAC-TTC-AGA-AAC-AGA (Seq. ID No. 42); GGC-CTC-AAA-GAC-GTT-TAA (Seq. ID No. 43); GTG-AAA-GTT-CCA-AGT-GAA (Seq. ID No. 44); GAG-TGC-TTT-GAA-GCC-TAC (Seq. ID No. 45); GAA-ACA-GCA-GAG-TTG-AAA (Seq. ID No. 46); TGC-AGA-GAT-CAC-AAC-GTG (Seq. ID No. 47); ACA-AAG-AAT-CAT-TCG-CAG (Seq. ID No. 48); AGT-GTT-AGA-AAA-CTG-CTC (Seq. ID No. 49); ACA-CGA-TTT-TGG-AAA-CAC (Seq. ID No. 119); CGA-AAC-ATC-ACT-GAG-AGT (Seq. ID No. 120); GGA-TGA-CAT-ATA-ATA-ACT-AG (Seq. ID No. 121); GAA-TTG-AAC-ATT-CAC-TTT-GA (Seq. ID No. 122); TAG-CTC-TGA-AGA-TTT-CGT (Seq. ID No. 123); GAG-ATG-TTT-CCG-AGA-ATG (Seq. ID No. 124); GTG-TAT-TCA-ACT-ACC-AGA (Seq. ID No. 125); ACA-TTT-CTG-TTA-CAG-AGC (Seq. ID No. 126); ATG-ACG-TAT-AAA-ATC-TAG-AG (Seq. ID No. 127); ACG-AAC-ACA-GTT-GAA-CCT (Seq. ID No. 128); CTC-ATA-AAA-ACC-AGA-AAG-AG (Seq. ID No. 129); CTG-TTC-AGA-GTA-ACA-TGA (Seq. ID No. 50); CCG-CTT-GGA-AAT-ACT-ACA (Seq. ID No. 51); GAA-ATG-GAA-ATA-TCT-CCC-C (Seq. ID No. 52); TCT-AGG-AGG-TCC-AAT-TAT (Seq. ID No. 53); GAA-TTC-CCA-AGT-GGA-TAT (Seq. ID No. 54); CTG-TAG-GTT-TAG-ATG-AAG (Seq. ID No. 55); AAG-GAG-

TGT-TTC-CCA-ACT (Seq. ID No. 56); GGC-TTC-AAG-GCG-CTC-TAA  
 (Seq. ID No. 57); GCA-GAG-ACT-TCA-AAG-TGC (Seq. ID No. 58); CAC-  
 ACA-CAC-GGT-GGA-CCA (Seq. ID No. 59); CAA-AGG-GAA-TGT-TCC-  
 ATT (Seq. ID No. 60); CAC-ATA-GCA-GTG-TTT-GAG (Seq. ID No. 61);  
 CTC-AAG-GCG-GTC-CAA-TTA (Seq. ID No. 62); GAG-TCG-AAA-TGC-  
 ACA-CAT (Seq. ID No. 63); TAC-CAA-GAG-GAA-TGT-TGC (Seq. ID No.  
 64); CAG-TTC-ATA-TGT-GCA-GTG (Seq. ID No. 130); GGA-ATA-TCG-  
 TCA-CCT-AAA (Seq. ID No. 131); TGG-AGC-AAA-TTG-AAG-CCT (Seq.  
 ID No. 132); TGG-AGC-ACA-TTT-ATG-CCT (Seq. ID No. 133); TGC-ATT-  
 CTA-CTC-CCA-TAG (Seq. ID No. 134); ACA-CTC-TGT-TTC-TAA-AAT-  
 CT (Seq. ID No. 135); GCA-GGC-GGA-TAT-TTA-GTA (Seq. ID No. 136);  
 AGC-GAT-TTG-ATG-CCA-ACA (Seq. ID No. 137); TTG-CAA-ACG-GGG-  
 TTT-CTT (Seq. ID No. 138); CTT-TCA-TGC-TAG-ACA-GAA (Seq. ID No.  
 139); CAA-AAA-AGT-TAC-TGA-GAA-C (Seq. ID No. 140); AAA-ATG-  
 CCA-CAG-CAA-GAG (Seq. ID No. 141); GTT-TGA-AAA-CAC-ACT-GTT-  
 TG (Seq. ID No. 142); ATA-TGG-ACC-TGT-TTG-AGG (Seq. ID No. 143);  
 CAT-TGA-ATG-CTA-GAC-GGA (Seq. ID No. 144); ACG-GGA-TGC-AAT-  
 ATA-AAA (Seq. ID No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No.  
 66); AAG-GTT-TGT-ACT-GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-  
 GGT-GAA-AAA (Seq. ID No. 68); ACT-AAC-TGT-GCT-GAA-CAT (Seq.  
 ID No. 69); CCC-ATG-AAT-GCG-AGA-TAG (Seq. ID No. 70); ATG-ATG-  
 AAA-AAG-GTA-ATA (Seq. ID No. 145); CAT-TCT-CAG-AAC-TGT-TTG  
 (Seq. ID No. 146); AAC-TGA-ACG-CAC-AGA-TGA (Seq. ID No. 71); GGC-  
 TAA-TCT-TTG-AAA-TTG-AAA (Seq. ID No. 72); AGG-TGG-ATA-ATT-  
 GGC-CCT (Seq. ID No. 73); TGA-AGT-CCA-AAA-AAG-CAC (Seq. ID No.  
 74); CTT-AGA-CAT-GGA-AAT-ATC (Seq. ID No. 75); AAG-GGG-TCT-  
 AAC-TAA-TCA (Seq. ID No. 76); GTA-GTT-GTT-GAG-AAT-GAT (Seq. ID  
 No. 77); AAC-TTC-CCA-GAA-CTA-CAC (Seq. ID No. 78); ATT-CTT-GAA-  
 ATG-GAA-CAC (Seq. ID No. 79); CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID  
 No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq. ID No. 81); GAA-ATT-  
 TCC-TGT-TGA-CAG-A (Seq. ID No. 82); GTT-TGA-AAG-CTG-AAC-TAT-

G (Seq. ID No. 83); TCC-TGT-AAT-GTT-CGA-CAG (Seq. ID No. 84); TCA-TAG-AAC-GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-AAG-GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID No. 87); GAG-TTG-AAT-AGA-GGC-AAC (Seq. ID No. 88); GGC-CAA-ATG-TAG-AAA-AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No. 92); GAA-TAC-TGA-GTA-AGT-TCT-TTG (Seq. ID No. 93); AAC-TGC-ACA-AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT (Seq. ID No. 95); CCA-GTT-GGA-GAT-TTC-AAT (Seq. ID No. 96); GAA-GCC-TGC-CAG-TGG-ATA (Seq. ID No. 97); TAC-AGC-ATT-CTG-GAA-ACC (Seq. ID No. 98); CCA-GAC-ACT-GCG-TAG-TGA (Seq. ID No. 99); ATA-TAA-TGC-TAG-AGG-GAG (Seq. ID No. 100); AAA-AAC-AAG-ACA-AAC-TCG (Seq. ID No. 101); ATT-TCA-GCT-GAC-TAA-ACA (Seq. ID No. 102); AAC-GAA-TTA-TGG-TCA-CAT (Seq. ID No. 103); GGT-GAC-GAC-TGA-GTT-TAA (Seq. ID No. 104); TTT-GGA-CCA-CTC-TGT-GGC (Seq. ID No. 105); AAC-GGG-ATA-ACT-GCA-CCT (Seq. ID No. 106); TTT-GTG-GTT-TGT-GGT-GGA (Seq. ID No. 107); AGG-GAA-TAG-CTT-CAT-AGA (Seq. ID No. 108); ATC-ACG-AAG-AAG-GTT-CTG (Seq. ID No. 109); CCG-AAG-ATG-TCT-TTG-GAA (Seq. ID No. 110); AAA-GAG-GTC-TAC-ATG-TCC (Seq. ID No. 111); TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115); ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116); GCA-CTT-ACC-GGC-CTA-AG (Seq. ID No. 117) and CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118); ACA-GAA-CTA-AAC-CAT-CGT (Seq. ID No. 147); TAG-GCC-AGC-TTG-GAG-GAT (Seq. ID No. 148); CTA-GCT-GGG-AGG-ATT-T (Seq. ID No. 149); TGT-GCC-TCA-ACT-GAC-A (Seq. ID No. 150); TGC-TTT-GGG-ATG-TTT-CAA (Seq. ID No. 151); GCA-ATG-TCA-GAA-CTT-TTT-TC (Seq. ID No. 152); CCG-AAA-GAA-ATT-TGT-GGG (Seq. ID No. 153); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 154); TCA-AGG-CGA-TCG-AAA-TGT (Seq.

ID No. 155); GAG-ACA-CAT-ATC-ACC-AAC (Seq. ID No. 156); CAG-AAA-TTT-CTT-TCG-GAT-A (Seq. ID No. 157); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 158) and AGC-CAA-AGG-AGT-TGA-ACA (Seq. ID No. 159), or the complement to any of the foregoing sequences.

Claims 22-23 (Canceled)

24. (Currently Amended; Withdrawn) The method of claim 23, wherein the presence, absence or number of human chromosome 4 in a sample is determined by:

- a) contacting the sample with one or more PNA probes of ~~10~~ up to 30 subunits in length, wherein at least one probe comprises a probing nucleobase sequence, ~~at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements,~~ selected from the group consisting of:  
 ACA-CGA-TTT-TGG-AAA-CAC (Seq. ID No. 119); CGA-AAC-ATC-ACT-GAG-AGT (Seq. ID No. 120); GGA-TGA-CAT-ATA-ATA-ACT-AG (Seq. ID No. 121); GAA-TTG-AAC-ATT-CAC-TTT-GA (Seq. ID No. 122); TAG-CTC-TGA-AGA-TTT-CGT (Seq. ID No. 123); GAG-ATG-TTT-CCG-AGA-ATG (Seq. ID No. 124); GTG-TAT-TCA-ACT-ACC-AGA (Seq. ID No. 125); ACA-TTT-CTG-TTA-CAG-AGC (Seq. ID No. 126); ATG-ACG-TAT-AAA-ATC-TAG-AG (Seq. ID No. 127); ACG-AAC-ACA-GTT-GAA-CCT (Seq. ID No. 128) and CTC-ATA-AAA-ACC-AGA-AAG-AG (Seq. ID No. 129), or the complement to any of the foregoing sequences; and
- b) detecting, identifying or quantitating hybridization of the probing nucleobase sequence of the probe or probes to a target sequence in the sample to thereby correlate the result with the presence, absence or number of human X chromosomes 4 in the sample.

25. (Currently Amended; Withdrawn) The method of claim 23, wherein the presence, absence or number of human chromosome 7 in a sample is determined by:

- a) contacting the sample with one or more PNA probes of ~~10~~ up to 30 subunits in length, wherein at least one probe comprises a probing nucleobase sequence, ~~at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements,~~ selected from the group consisting of:

CAG-TTC-ATA-TGT-GCA-GTG (Seq. ID No. 130); GGA-ATA-TCG-TCA-CCT-AAA (Seq. ID No. 131); TGG-AGC-AAA-TTG-AAG-CCT (Seq. ID No. 132); TGG-AGC-ACA-TTT-ATG-CCT (Seq. ID No. 133); TGC-ATT-CTA-CTC-CCA-TAG (Seq. ID No. 134); ACA-CTC-TGT-TTC-TAA-AAT-CT (Seq. ID No. 135); GCA-GGC-GGA-TAT-TTA-GTA (Seq. ID No. 136); AGC-GAT-TTG-ATG-CCA-ACA (Seq. ID No. 137); TTG-CAA-ACG-GGG-TTT-CTT (Seq. ID No. 138); CTT-TCA-TGC-TAG-ACA-GAA (Seq. ID No. 139); CAA-AAA-AGT-TAC-TGA-GAA-C (Seq. ID No. 140); AAA-ATG-CCA-CAG-CAA-GAG (Seq. ID No. 141); GTT-TGA-AAA-CAC-ACT-GTT-TG (Seq. ID No. 142); ATA-TGG-ACC-TGT-TTG-AGG (Seq. ID No. 143); and CAT-TGA-ATG-CTA-GAC-GGA (Seq. ID No. 144), or the complement to any of the foregoing sequences; and

- b) detecting, identifying or quantitating hybridization of the probing nucleobase sequence of the probe or probes to a target sequence in the sample to thereby correlate the result with the presence, absence or number of human  $\forall$  chromosomes 7 in the sample.

26. (Currently Amended; Withdrawn) The method of claim 23, wherein the presence, absence or number of human chromosome 9 in a sample is determined by:

- a) contacting the sample with one or more PNA probes of ~~10~~ up to 30 subunits in length, wherein at least one probe comprises a probing

nucleobase sequence, ~~at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements,~~ selected from the group consisting of:

ATG-ATG-AAA-AAG-GTA-ATA (Seq. ID No. 145) and CAT-TCT-CAG-AAC-TGT-TTG (Seq. ID No. 146), or the complement to any of the foregoing sequences; and

- b) detecting, identifying or quantitating hybridization of the probing nucleobase sequence of the probe or probes to a target sequence in the sample to thereby correlate the result with the presence, absence or number of human chromosome ~~19~~ in the sample.

27. (Currently Amended; Withdrawn) The method of claim 23, wherein the presence, absence or number of human chromosome 20 in a sample is determined by:

- a) contacting the sample with one or more PNA probes of ~~10~~ up to 30 subunits in length, wherein at least one probe comprises a probing nucleobase sequence, ~~at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements,~~ selected from the group consisting of:

ACA-GAA-CTA-AAC-CAT-CGT (Seq. ID No. 147); TAG-GCC-AGC-TTG-GAG-GAT (Seq. ID No. 148); CTA-GCT-GGG-AGG-ATT-T (Seq. ID No. 149); TGT-GCC-TCA-ACT-GAC-A (Seq. ID No. 150); TGC-TTT-GGG-ATG-TTT-CAA (Seq. ID No. 151); and GCA-ATG-TCA-GAA-CTT-TTT-TC (Seq. ID No. 152), or the complement to any of the foregoing sequences; and

- b) detecting, identifying or quantitating hybridization of the probing nucleobase sequence of the probe or probes to a target sequence in the sample to thereby correlate the result with the presence, absence or number of human chromosome 20 in the sample.

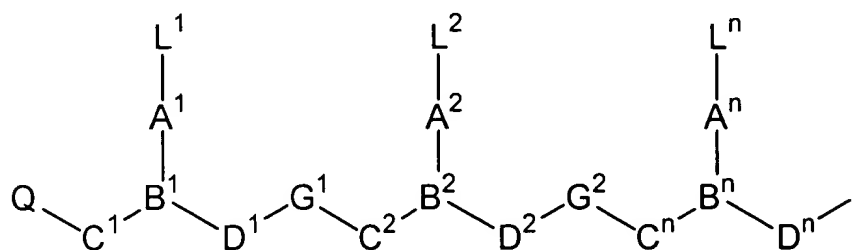


28. (Currently Amended; Withdrawn) The method of claim 23, wherein the presence, absence or number of human chromosomes 13 and 21 as a pair in a sample is determined by:
- a) contacting the sample with one or more PNA probes of ~~10~~ up to 30 subunits in length, wherein at least one probe comprises a probing nucleobase sequence, ~~at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements,~~ selected from the group consisting of:  
 CCG-AAA-GAA-ATT-TGT-GGG (Seq. ID No. 153); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 154); TCA-AGG-CGA-TCG-AAA-TGT (Seq. ID No. 155); GAG-ACA-CAT-ATC-ACC-AAC (Seq. ID No. 156); CAG-AAA-TTT-CTT-TCG-GAT-A (Seq. ID No. 157); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 158) and AGC-CAA-AGG-AGT-TGA-ACA (Seq. ID No. 159), or the complement to any of the foregoing sequences; and
  - b) detecting, identifying or quantitating hybridization of the probing nucleobase sequence of the probe or probes to a target sequence in the sample to thereby correlate the result with the presence, absence or number of human chromosomes ~~3~~ 13 and 21 in the sample.
29. (Previously Amended) The method of claim 21, wherein *in-situ* hybridization is used to detect, identify or enumerate human chromosomes X, Y, 1, 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 16, 17, 18 and 20, as well as 13/21 as a pair, in the sample.
30. (Previously Amended) The method of claim 21, wherein the method is used to detect or identify chromosome related abnormalities.
31. (Previously Amended) The method of claim 21, wherein the method is used to detect abnormalities in cells, tissues (including bone marrow), spermatozoa, ova, blastomeres, oocysts, buccal cells and chorionic villi.

32. (Original) The method of claim 31, wherein the chromosome related abnormality is aneuploidy or polyploidy.
33. (Original) The method of claim 31, wherein the method is used in preimplantation diagnosis or in prenatal screening.

Claim 34 (Canceled)

35. (Currently Amended) A set of at least four PNA probes of up to 30 subunits in length wherein said PNA probes have the formula:



wherein,

n is at least 2,

each of  $L^1$ - $L^n$  is independently selected from the group consisting of hydrogen, hydroxy,  $(C_1-C_4)$ alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of  $C^1$ - $C^n$  is  $(CR^6R^7)_y$ , where  $R^6$  is hydrogen and  $R^7$  is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or  $R^6$  and  $R^7$  are independently selected from the group consisting of hydrogen,  $(C_2-C_6)$ alkyl, aryl, aralkyl, heteroaryl, hydroxy,  $(C_1-C_6)$ alkoxy,  $(C_1-C_6)$ alkylthio,  $NR^3R^4$  and  $SR^5$ , where  $R^3$  and  $R^4$  are as defined above, and  $R^5$  is hydrogen,  $(C_1-C_6)$ alkyl, hydroxy-, alkoxy-, or alkylthio- substituted  $(C_1-C_6)$ alkyl, or  $R^6$  and  $R^7$  taken together complete an alicyclic or heterocyclic system;

each of  $D^1$ - $D^n$  is  $(CR^6R^7)_z$ , where  $R^6$  and  $R^7$  are as defined above;

each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

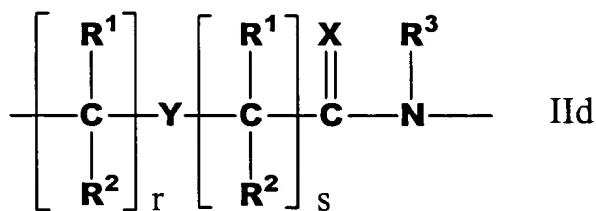
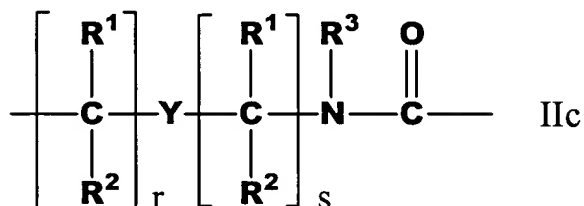
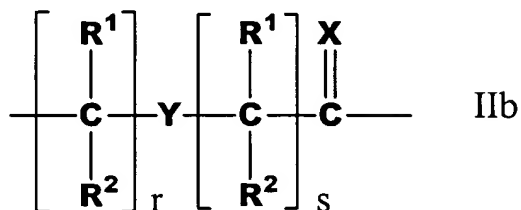
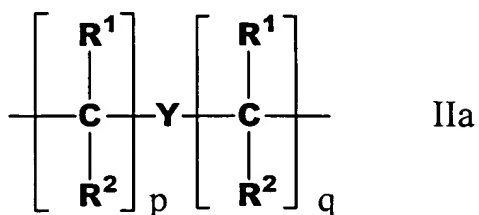
each of  $G^1-G^{n-1}$  is  $-NR^3CO-$ ,  $-NR^3CS-$ ,  $-NR^3SO-$  or  $-NR^3SO_2-$ , in either orientation,

where  $R^3$  is as defined above;

each of  $A^1-A^n$  and  $B^1-B^n$  are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (IIId), and B is N or  $R^3N^+$ ; or

(b) A is a group of formula (IIId) and B is CH;



where:

X is O, S, Se,  $NR^3$ ,  $CH_2$  or  $C(CH_3)_2$ ;

Y is a single bond, O, S or  $NR^4$ ;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each  $R^1$  and  $R^2$  is independently selected from the group consisting of hydrogen,  $(C_1-C_4)$ alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each  $R^3$  and  $R^4$  is independently selected from the group consisting of hydrogen,  $(C_1-C_4)$ alkyl, hydroxy- or alkoxy- or alkylthio-substituted  $(C_1-C_4)$ alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is  $-CO_2H$ ,  $-CONR'R''$ ,  $-SO_3H$  or  $-SO_2NR'R''$  or an activated derivative of  $-CO_2H$  or  $-SO_3H$ ; and

I is  $-NHR'''R''''$  or  $-NR'''C(O)R''''$ , where  $R'$ ,  $R''$ ,  $R'''$  and  $R''''$  are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids; and wherein:  
~~the one or more~~ of the PNA probes of the set is specific for detecting human chromosome X and ~~comprises~~ a probing nucleobase sequence selected from the group consisting of:

CTT-CAA-AGA-GGT-CCA-CGA (Seq. ID No. 1); AGG-GTT-CAA-CTG-TGT-GAC (Seq. ID No. 2); GAA-ACT-TCT-GAG-TGA-TGA (Seq. ID No. 3); CAG-TCA-TCG-CAG-AAA-ACT (Seq. ID No. 4); AGA-TTT-CAC-TGG-AAA-CGG (Seq. ID No. 5); GTT-ATG-GGA-AGG-TGA-TCC (Seq. ID No. 6); TCG-AGC-CGC-AGA-GTT-TAA (Seq. ID No. 7); CTA-TTT-AGC-GGG-CTT-GGA (Seq. ID No. 8) and TAC-AAG-GGT-GTT-GCA-AAC (Seq. ID No. 9), or the complement to any of the foregoing sequences;

~~the one or more~~ of the PNA probes of the set is specific for detecting human chromosome Y and ~~comprises~~ a probing nucleobase sequence selected from the group consisting of:

CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT

(Seq. ID No. 15) and GGC-ATA-GCA-CAT-AAC-ATG (Seq. ID No. 16), or the complement to any of the foregoing sequences; ~~the~~ one or more of the PNA probes of the set is specific for detecting human chromosome 18 and comprises a probing nucleobase sequence selected from the group consisting of:

TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115); ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116); GCA-CTT-ACC-GGC-CTA-AG (Seq. ID No. 117) and CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118) or the complement to any of the foregoing sequences;

~~the~~ one or more of the PNA probes of the set is specific for detecting human chromosome 13/21 and comprises a probing nucleobase sequence selected from the group consisting of:

CCG-AAA-GAA-ATT-TGT-GGG (Seq. ID No. 153); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 154); TCA-AGG-CGA-TCG-AAA-TGT (Seq. ID No. 155); GAG-ACA-CAT-ATC-ACC-AAC (Seq. ID No. 156); CAG-AAA-TTT-CTT-TCG-GAT-A (Seq. ID No. 157); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 158) and AGC-CAA-AGG-AGT-TGA-ACA (Seq. ID No. 159), or the complement to any of the foregoing sequences.

36. (Currently Amended) A kit for performing an assay comprising:

- a) one or more PNA probes of up to 30 subunits in length wherein at least one probe comprises a probing nucleobase sequence selected from the group consisting of: CTT-CAA-AGA-GGT-CCA-CGA (Seq. ID No. 1); AGG-GTT-CAA-CTG-TGT-GAC (Seq. ID No. 2); GAA-ACT-TCT-GAG-TGA-TGA (Seq. ID No. 3); CAG-TCA-TCG-CAG-AAA-ACT (Seq. ID No. 4); AGA-TTT-CAC-TGG-AAA-CGG (Seq. ID No. 5); GTT-ATG-GGA-AGG-TGA-TCC (Seq. ID No. 6); TCG-AGC-CGC-AGA-GTT-TAA (Seq. ID No. 7); CTA-TTT-AGC-

GGG-CTT-GGA (Seq. ID No. 8); TAC-AAG-GGT-GTT-GCA-AAC (Seq. ID No. 9); CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT (Seq. ID No. 15); GGC-ATA-GCA-CAT-AAC-ATG (Seq. ID No. 16); AAT-CGT-CAT-CGA-ATG-AAT (Seq. ID No. 17); CAT-TGA-ACA-GAA-TTG-AAT (Seq. ID No. 18); GTT-TTC-AGG-GGA-AGA-TAT (Seq. ID No. 19); TGT-GCG-CCC-TCA-ACT-AAC (Seq. ID No. 20); GAA-GCT-TCA-TTG-GGA-TGT (Seq. ID No. 21); CCA-ATA-AAA-GCT-ACA-TAG-A (Seq. ID No. 22); GAA-AAA-GTT-TCT-GAC-ATT-GC (Seq. ID No. 23); TAG-TTG-AAG-GGC-ACA-TCA (Seq. ID No. 24); CAC-AAA-TAA-GAT-TCT-AAG-AAT (Seq. ID No. 25); TCA-AAA-GAA-TGC-TTC-AAC-AC (Seq. ID No. 26); ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27); GCT-GTT-TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-AGG-TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID No. 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-TCA-ACT-CAC-GGA (Seq. ID No. 32); CCT-CAC-AAA-GTA-GAA-ACT (Seq. ID No. 33); GAA-AAA-GCA-GTT-ACT-GAG (Seq. ID No. 34); TAA-TAA-TTA-GAC-GGA-ATC-AT (Seq. ID No. 35); TTA-CAG-GGC-ATT-GAA-GCC (Seq. ID No. 36); CAG-TTA-TGA-AGC-AGT-CTC (Seq. ID No. 37); CAC-ACC-AGA-AAA-AGC-AGT (Seq. ID No. 38); AAG-GGT-AAA-CAC-TGT-GAG (Seq. ID No. 39); AGA-CAA-CGA-AAT-ATC-TTC-ATG (Seq. ID No. 40); CTA-GCA-GTA-TGA-GGT-CAA (Seq. ID No. 41); GCA-GAC-TTC-AGA-AAC-AGA (Seq. ID No. 42); GGC-CTC-AAA-GAC-GTT-TAA (Seq. ID No. 43); GTG-AAA-GTT-CCA-AGT-GAA (Seq. ID No. 44); GAG-TGC-TTT-GAA-GCC-TAC (Seq. ID No. 45); GAA-ACA-GCA-GAG-TTG-AAA (Seq. ID No. 46); TGC-AGA-GAT-CAC-AAC-GTG (Seq. ID No. 47); ACA-AAG-AAT-CAT-TCG-CAG (Seq. ID No. 48); AGT-GTT-AGA-AAA-CTG-CTC (Seq. ID No. 49); ACA-CGA-TTT-TGG-AAA-CAC (Seq. ID No. 119); CGA-AAC-ATC-ACT-GAG-AGT (Seq. ID No. 120); GGA-TGA-CAT-ATA-ATA-ACT-

AG (Seq. ID No. 121); GAA-TTG-AAC-ATT-CAC-TTT-GA (Seq. ID No. 122);  
 TAG-CTC-TGA-AGA-TTT-CGT (Seq. ID No. 123); GAG-ATG-TTT-CCG-  
 AGA-ATG (Seq. ID No. 124); GTG-TAT-TCA-ACT-ACC-AGA (Seq. ID No.  
 125); ACA-TTT-CTG-TTA-CAG-AGC (Seq. ID No. 126); ATG-ACG-TAT-  
 AAA-ATC-TAG-AG (Seq. ID No. 127); ACG-AAC-ACA-GTT-GAA-CCT  
 (Seq. ID No. 128); CTC-ATA-AAA-ACC-AGA-AAG-AG (Seq. ID No. 129);  
 CTG-TTC-AGA-GTA-ACA-TGA (Seq. ID No. 50); CCG-CTT-GGA-AAT-  
 ACT-ACA (Seq. ID No. 51); GAA-ATG-GAA-ATA-TCT-CCC-C (Seq. ID No.  
 52); TCT-AGG-AGG-TCC-AAT-TAT (Seq. ID No. 53); GAA-TTC-CCA-AGT-  
 GGA-TAT (Seq. ID No. 54); CTG-TAG-GTT-TAG-ATG-AAG (Seq. ID No.  
 55); AAG-GAG-TGT-TTC-CCA-ACT (Seq. ID No. 56); GGC-TTC-AAG-GCG-  
 CTC-TAA (Seq. ID No. 57); GCA-GAG-ACT-TCA-AAG-TGC (Seq. ID No.  
 58); CAC-ACA-CAC-GGT-GGA-CCA (Seq. ID No. 59); CAA-AGG-GAA-  
 TGT-TCC-ATT (Seq. ID No. 60); CAC-ATA-GCA-GTG-TTT-GAG (Seq. ID  
 No. 61); CTC-AAG-GCG-GTC-CAA-TTA (Seq. ID No. 62); GAG-TCG-AAA-  
 TGC-ACA-CAT (Seq. ID No. 63); TAC-CAA-GAG-GAA-TGT-TGC (Seq. ID  
 No. 64); CAG-TTC-ATA-TGT-GCA-GTG (Seq. ID No. 130); GGA-ATA-TCG-  
 TCA-CCT-AAA (Seq. ID No. 131); TGG-AGC-AAA-TTG-AAG-CCT (Seq. ID  
 No. 132); TGG-AGC-ACA-TTT-ATG-CCT (Seq. ID No. 133); TGC-ATT-CTA-  
 CTC-CCA-TAG (Seq. ID No. 134); ACA-CTC-TGT-TTC-TAA-AAT-CT (Seq.  
 ID No. 135); GCA-GGC-GGA-TAT-TTA-GTA (Seq. ID No. 136); AGC-GAT-  
 TTG-ATG-CCA-ACA (Seq. ID No. 137); TTG-CAA-ACG-GGG-TTT-CTT  
 (Seq. ID No. 138); CTT-TCA-TGC-TAG-ACA-GAA (Seq. ID No. 139); CAA-  
 AAA-AGT-TAC-TGA-GAA-C (Seq. ID No. 140); AAA-ATG-CCA-CAG-  
 CAA-GAG (Seq. ID No. 141); GTT-TGA-AAA-CAC-ACT-GTT-TG (Seq. ID  
 No. 142); ATA-TGG-ACC-TGT-TTG-AGG (Seq. ID No. 143); CAT-TGA-  
 ATG-CTA-GAC-GGA (Seq. ID No. 144); ACG-GGA-TGC-AAT-ATA-AAA  
 (Seq. ID No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No. 66); AAG-  
 GTT-TGT-ACT-GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-GGT-GAA-  
 AAA (Seq. ID No. 68); ACT-AAC-TGT-GCT-GAA-CAT (Seq. ID No. 69);  
 CCC-ATG-AAT-GCG-AGA-TAG (Seq. ID No. 70); ATG-ATG-AAA-AAG-

GTA-ATA (Seq. ID No. 145); CAT-TCT-CAG-AAC-TGT-TTG (Seq. ID No. 146); TAA-AAA-GAA-AGG-TTC-ATC (Seq. ID No. 147); GCT-TGC-AGA-TAC-TAC-AGA (Seq. ID No. 148); TGA-AAG-CGC-TTA-AAA-CGT (Seq. ID No. 149); AAC-TGA-ACG-CAC-AGA-TGA (Seq. ID No. 71); GGC-TAA-TCT-TTG-AAA-TTG-AAA (Seq. ID No. 72); AGG-TGG-ATA-ATT-GGC-CCT (Seq. ID No. 73); TGA-AGT-CCA-AAA-AAG-CAC (Seq. ID No. 74); CTT-AGA-CAT-GGA-AAT-ATC (Seq. ID No. 75); AAG-GGG-TCT-AAC-TAA-TCA (Seq. ID No. 76); GTA-GTT-GTT-GAG-AAT-GAT (Seq. ID No. 77); AAC-TTC-CCA-GAA-CTA-CAC (Seq. ID No. 78); ATT-CTT-GAA-ATG-GAA-CAC (Seq. ID No. 79); CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq. ID No. 81); GAA-ATT-TCC-TGT-TGA-CAG-A (Seq. ID No. 82); GTT-TGA-AAG-CTG-AAC-TAT-G (Seq. ID No. 83); TCC-TGT-AAT-GTT-CGA-CAG (Seq. ID No. 84); TCA-TAG-AAC-GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-AAG-GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID No. 87); GAG-TTG-AAT-AGA-GGC-AAC (Seq. ID No. 88); GGC-CAA-ATG-TAG-AAA-AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No. 92); GAA-TAC-TGA-GTA-AGT-TCT-TTG (Seq. ID No. 93); AAC-TGC-ACA-AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT (Seq. ID No. 95); CCA-GTT-GGA-GAT-TTC-AAT (Seq. ID No. 96); GAA-GCC-TGC-CAG-TGG-ATA (Seq. ID No. 97); TAC-AGC-ATT-CTG-GAA-ACC (Seq. ID No. 98); CCA-GAC-ACT-GCG-TAG-TGA (Seq. ID No. 99); ATA-TAA-TGC-TAG-AGG-GAG (Seq. ID No. 100); AAA-AAC-AAG-ACA-AAC-TCG (Seq. ID No. 101); ATT-TCA-GCT-GAC-TAA-ACA (Seq. ID No. 102); AAC-GAA-TTA-TGG-TCA-CAT (Seq. ID No. 103); GGT-GAC-GAC-TGA-GTT-TAA (Seq. ID No. 104); TTT-GGA-CCA-CTC-TGT-GGC (Seq. ID No. 105); AAC-GGG-ATA-ACT-GCA-CCT (Seq. ID No. 106); TTT-GTG-GTT-TGT-GGT-GGA (Seq. ID No. 107); AGG-GAA-TAG-CTT-CAT-AGA (Seq. ID No. 108); ATC-ACG-AAG-AAG-GTT-CTG (Seq. ID No. 109); CCG-AAG-ATG-TCT-TTG-GAA (Seq. ID No. 110); AAA-GAG-



GTC-TAC-ATG-TCC (Seq. ID No. 111); TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115); ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116); GCA-CTT-ACC-GGC-CTA-AG (Seq. ID No. 117); CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118); ACA-GAA-CTA-AAC-CAT-CGT (Seq. ID No. 147); TAG-GCC-AGC-TTG-GAG-GAT (Seq. ID No. 148); CTA-GCT-GGG-AGG-ATT-T (Seq. ID No. 149); TGT-GCC-TCA-ACT-GAC-A (Seq. ID No. 150); TGC-TTT-GGG-ATG-TTT-CAA (Seq. ID No. 151); GCA-ATG-TCA-GAA-CTT-TTT-TC (Seq. ID No. 152); CCG-AAA-GAA-ATT-TGT-GGG (Seq. ID No. 153); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 157); TCA-AGG-CGA-TCG-AAA-TGT (Seq. ID No. 158); GAG-ACA-CAT-ATC-ACC-AAC (Seq. ID No. 159); CAG-AAA-TTT-CTT-TCG-GAT-A (Seq. ID No. 157); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 158); AGC-CAA-AGG-AGT-TGA-ACA (Seq. ID No. 159), or the complement to any of the foregoing sequences; and

b) other reagents or compositions necessary to perform the assay.

37. (Previously Amended) The kit of claim 36, wherein the probe or probes are unlabeled.

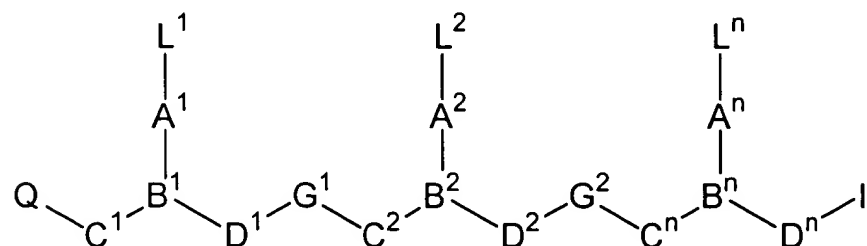
38. (Currently Amended) The kit of claim 37, wherein ~~hybridization of the probing nucleobase sequence of the probe to the chromosome is detected using the kit~~ further comprises an antibody or antibody fragment, wherein the antibody or antibody fragment specifically binds, under antibody binding conditions, to the PNA/nucleic acid complex which forms under suitable hybridization conditions.

39. (Original) The kit of claim 38, comprising an antibody labeled with a detectable moiety.

40. (Original) The kit of claim 39, wherein the detectable moiety is selected from the group consisting of a dextran conjugate, a branched nucleic acid detection system, a chromophore, a fluorophore, a spin label, a radioisotope, an enzyme, a hapten, an acridinium ester and a chemiluminescent compound.
41. (Previously Amended) The kit of claim 36, wherein at least one PNA probe is labeled with a detectable moiety.
42. (Original) The kit of claim 41, wherein the detectable moiety or moieties are selected from the group consisting of: a dextran conjugate, a branched nucleic acid detection system, a chromophore, a fluorophore, a spin label, a radioisotope, an enzyme, a hapten, an acridinium ester and a chemiluminescent compound.

Claims 43-44 (Canceled)

45. (Currently Amended) A prenatal kit for the multiplex analysis of human chromosomes X, Y, 13, 18 and 21, wherein the kit comprises independently detectable PNA probes of up to 30 subunits in length for the individual detection of human chromosomes X, Y, 18, as well as human chromosomes 13 and 21 as a pair, and other reagents or components suitable to perform an assay wherein said PNA probes have the formula:



wherein,

n is at least 2,

each of  $L^1$ - $L^n$  is independently selected from the group consisting of hydrogen, hydroxy,  $(C_1-C_4)$ alkanoyl, naturally occurring nucleobases, aromatic moieties,

DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of  $C^1-C^n$  is  $(CR^6R^7)_y$ , where  $R^6$  is hydrogen and  $R^7$  is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or  $R^6$  and  $R^7$  are independently selected from the group consisting of hydrogen,  $(C_2-C_6)$ alkyl, aryl, aralkyl, heteroaryl, hydroxy,  $(C_1-C_6)$ alkoxy,  $(C_1-C_6)$ alkylthio,  $NR^3R^4$  and  $SR^5$ , where  $R^3$  and  $R^4$  are as defined above, and  $R^5$  is hydrogen,  $(C_1-C_6)$ alkyl, hydroxy-, alkoxy-, or alkylthio- substituted  $(C_1-C_6)$ alkyl, or  $R^6$  and  $R^7$  taken together complete an alicyclic or heterocyclic system;

each of  $D^1-D^n$  is  $(CR^6R^7)_z$  where  $R^6$  and  $R^7$  are as defined above;

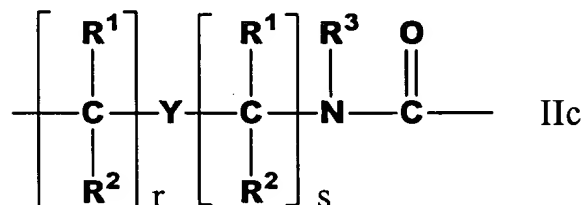
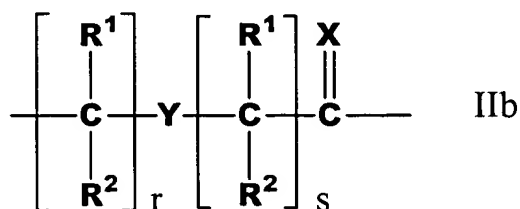
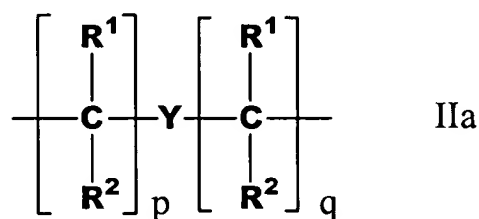
each of  $y$  and  $z$  is zero or an integer from 1 to 10, the sum  $y+z$  being greater than 2 but not more than 10;

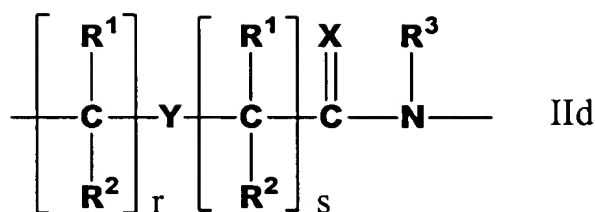
each of  $G^1-G^{n-1}$  is  $-NR^3CO-$ ,  $-NR^3CS-$ ,  $-NR^3SO-$  or  $-NR^3SO_2-$ , in either orientation, where  $R^3$  is as defined above;

each of  $A^1-A^n$  and  $B^1-B^n$  are selected such that:

(a)  $A$  is a group of the formula (IIa), (IIb), (IIc), or (IId), and  $B$  is  $N$  or  $R^3N^+$ ; or

(b)  $A$  is a group of formula (IId) and  $B$  is  $CH$ ;





where:

X is O, S, Se, NR<sup>3</sup>, CH<sub>2</sub> or C(CH<sub>3</sub>)<sub>2</sub>;

Y is a single bond, O, S or NR<sup>4</sup>;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R<sup>1</sup> and R<sup>2</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R<sup>3</sup> and R<sup>4</sup> is independently selected from the group consisting of hydrogen, (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C<sub>1</sub>-C<sub>4</sub>)alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is -CO<sub>2</sub>H, -CONR'R'', -SO<sub>3</sub>H or -SO<sub>2</sub>NR'R'' or an activated derivative of -CO<sub>2</sub>H or -SO<sub>3</sub>H; and

I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids; and wherein:

the PNA probes comprise a probing nucleobase sequence-selected from the group consisting of:

CTT-CAA-AGA-GGT-CCA-CGA (Seq. ID No. 1); AGG-GTT-CAA-CTG-TGT-GAC (Seq. ID No. 2); GAA-ACT-TCT-GAG-TGA-TGA (Seq. ID No. 3); CAG-TCA-TCG-CAG-AAA-ACT (Seq. ID No. 4); AGA-TTT-CAC-TGG-AAA-CGG (Seq. ID No. 5); GTT-ATG-GGA-AGG-TGA-TCC (Seq. ID No. 6); TCG-AGC-CGC-AGA-GTT-TAA (Seq. ID No. 7); CTA-TTT-AGC-GGG-CTT-GGA (Seq. ID No. 8); TAC-AAG-GGT-GTT-GCA-AAC

(Seq. ID No. 9); CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT (Seq. ID No. 15); GGC-ATA-GCA-CAT-AAC-ATG (Seq. ID No. 16); AAT-CGT-CAT-CGA-ATG-AAT (Seq. ID No. 17); CAT-TGA-ACA-GAA-TTG-AAT (Seq. ID No. 18); GTT-TTC-AGG-GGA-AGA-TAT (Seq. ID No. 19); TGT-GCG-CCC-TCA-ACT-AAC (Seq. ID No. 20); GAA-GCT-TCA-TTG-GGA-TGT (Seq. ID No. 21); CCA-ATA-AAA-GCT-ACA-TAG-A (Seq. ID No. 22); GAA-AAA-GTT-TCT-GAC-ATT-GC (Seq. ID No. 23); TAG-TTG-AAG-GGC-ACA-TCA (Seq. ID No. 24); CAC-AAA-TAA-GAT-TCT-AAG-AAT (Seq. ID No. 25); TCA-AAA-GAA-TGC-TTC-AAC-AC (Seq. ID No. 26); ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27); GCT-GTT-TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-AGG-TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID No. 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-TCA-ACT-CAC-GGA (Seq. ID No. 32); CCT-CAC-AAA-GTA-GAA-ACT (Seq. ID No. 33); GAA-AAA-GCA-GTT-ACT-GAG (Seq. ID No. 34); TAA-TAA-TTA-GAC-GGA-ATC-AT (Seq. ID No. 35); TTA-CAG-GGC-ATT-GAA-GCC (Seq. ID No. 36); CAG-TTA-TGA-AGC-AGT-CTC (Seq. ID No. 37); CAC-ACC-AGA-AAA-AGC-AGT (Seq. ID No. 38); AAG-GGT-AAA-CAC-TGT-GAG (Seq. ID No. 39); AGA-CAA-CGA-AAT-ATC-TTC-ATG (Seq. ID No. 40); CTA-GCA-GTA-TGA-GGT-CAA (Seq. ID No. 41); GCA-GAC-TTC-AGA-AAC-AGA (Seq. ID No. 42); GGC-CTC-AAA-GAC-GTT-TAA (Seq. ID No. 43); GTG-AAA-GTT-CCA-AGT-GAA (Seq. ID No. 44); GAG-TGC-TTT-GAA-GCC-TAC (Seq. ID No. 45); GAA-ACA-GCA-GAG-TTG-AAA (Seq. ID No. 46); TGC-AGA-GAT-CAC-AAC-GTG (Seq. ID No. 47); ACA-AAG-AAT-CAT-TCG-CAG (Seq. ID No. 48); AGT-GTT-AGA-AAA-CTG-CTC (Seq. ID No. 49); ACA-CGA-TTT-TGG-AAA-CAC (Seq. ID No. 119); CGA-AAC-ATC-ACT-GAG-AGT (Seq. ID No.

120); GGA-TGA-CAT-ATA-ATA-ACT-AG (Seq. ID No. 121); GAA-TTG-AAC-ATT-CAC-TTT-GA (Seq. ID No. 122); TAG-CTC-TGA-AGA-TTT-CGT (Seq. ID No. 123); GAG-ATG-TTT-CCG-AGA-ATG (Seq. ID No. 124); GTG-TAT-TCA-ACT-ACC-AGA (Seq. ID No. 125); ACA-TTT-CTG-TTA-CAG-AGC (Seq. ID No. 126); ATG-ACG-TAT-AAA-ATC-TAG-AG (Seq. ID No. 127); ACG-AAC-ACA-GTT-GAA-CCT (Seq. ID No. 128); CTC-ATA-AAA-ACC-AGA-AAG-AG (Seq. ID No. 129); CTG-TTC-AGA-GTA-ACA-TGA (Seq. ID No. 50); CCG-CTT-GGA-AAT-ACT-ACA (Seq. ID No. 51); GAA-ATG-GAA-ATA-TCT-CCC-C (Seq. ID No. 52); TCT-AGG-AGG-TCC-AAT-TAT (Seq. ID No. 53); GAA-TTC-CCA-AGT-GGA-TAT (Seq. ID No. 54); CTG-TAG-GTT-TAG-ATG-AAG (Seq. ID No. 55); AAG-GAG-TGT-TTC-CCA-ACT (Seq. ID No. 56); GGC-TTC-AAG-GCG-CTC-TAA (Seq. ID No. 57); GCA-GAG-ACT-TCA-AAG-TGC (Seq. ID No. 58); CAC-ACA-CAC-GGT-GGA-CCA (Seq. ID No. 59); CAA-AGG-GAA-TGT-TCC-ATT (Seq. ID No. 60); CAC-ATA-GCA-GTG-TTT-GAG (Seq. ID No. 61); CTC-AAG-GCG-GTC-CAA-TTA (Seq. ID No. 62); GAG-TCG-AAA-TGC-ACA-CAT (Seq. ID No. 63); TAC-CAA-GAG-GAA-TGT-TGC (Seq. ID No. 64); CAG-TTC-ATA-TGT-GCA-GTG (Seq. ID No. 130); GGA-ATA-TCG-TCA-CCT-AAA (Seq. ID No. 131); TGG-AGC-AAA-TTG-AAG-CCT (Seq. ID No. 132); TGG-AGC-ACA-TTT-ATG-CCT (Seq. ID No. 133); TGC-ATT-CTA-CTC-CCA-TAG (Seq. ID No. 134); ACA-CTC-TGT-TTC-TAA-AAT-CT (Seq. ID No. 135); GCA-GGC-GGA-TAT-TTA-GTA (Seq. ID No. 136); AGC-GAT-TTG-ATG-CCA-ACA (Seq. ID No. 137); TTG-CAA-ACG-GGG-TTT-CTT (Seq. ID No. 138); CTT-TCA-TGC-TAG-ACA-GAA (Seq. ID No. 139); CAA-AAA-AGT-TAC-TGA-GAA-C (Seq. ID No. 140); AAA-ATG-CCA-CAG-CAA-GAG (Seq. ID No. 141); GTT-TGA-AAA-CAC-ACT-GTT-TG (Seq. ID No. 142); ATA-TGG-ACC-TGT-TTG-AGG (Seq. ID No. 143); CAT-TGA-ATG-CTA-GAC-GGA (Seq. ID No. 144); ACG-GGA-TGC-AAT-ATA-AAA (Seq. ID No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No. 66); AAG-GTT-TGT-ACT-GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-GGT-GAA-AAA (Seq. ID

No. 68); ACT-AAC-TGT-GCT-GAA-CAT (Seq. ID No. 69); CCC-ATG-AAT-GCG-AGA-TAG (Seq. ID No. 70); ATG-ATG-AAA-AAG-GTA-ATA (Seq. ID No. 145); CAT-TCT-CAG-AAC-TGT-TTG (Seq. ID No. 146); AAC-TGA-ACG-CAC-AGA-TGA (Seq. ID No. 71); GGC-TAA-TCT-TTG-AAA-TTG-AAA (Seq. ID No. 72); AGG-TGG-ATA-ATT-GGC-CCT (Seq. ID No. 73); TGA-AGT-CCA-AAA-AAG-CAC (Seq. ID No. 74); CTT-AGA-CAT-GGA-AAT-ATC (Seq. ID No. 75); AAG-GGG-TCT-AAC-TAA-TCA (Seq. ID No. 76); GTA-GTT-GTT-GAG-AAT-GAT (Seq. ID No. 77); AAC-TTC-CCA-GAA-CTA-CAC (Seq. ID No. 78); ATT-CTT-GAA-ATG-GAA-CAC (Seq. ID No. 79); CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq. ID No. 81); GAA-ATT-TCC-TGT-TGA-CAG-A (Seq. ID No. 82); GTT-TGA-AAG-CTG-AAC-TAT-G (Seq. ID No. 83); TCC-TGT-AAT-GTT-CGA-CAG (Seq. ID No. 84); TCA-TAG-AAC-GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-AAG-GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID No. 87); GAG-TTG-AAT-AGA-GGC-AAC (Seq. ID No. 88); GGC-CAA-ATG-TAG-AAA-AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No. 92); GAA-TAC-TGA-GTA-AGT-TCT-TTG (Seq. ID No. 93); AAC-TGC-ACA-AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT (Seq. ID No. 95); CCA-GTT-GGA-GAT-TTC-AAT (Seq. ID No. 96); GAA-GCC-TGC-CAG-TGG-ATA (Seq. ID No. 97); TAC-AGC-ATT-CTG-GAA-ACC (Seq. ID No. 98); CCA-GAC-ACT-GCG-TAG-TGA (Seq. ID No. 99); ATA-TAA-TGC-TAG-AGG-GAG (Seq. ID No. 100); AAA-AAC-AAG-ACA-AAC-TCG (Seq. ID No. 101); ATT-TCA-GCT-GAC-TAA-ACA (Seq. ID No. 102); AAC-GAA-TTA-TGG-TCA-CAT (Seq. ID No. 103); GGT-GAC-GAC-TGA-GTT-TAA (Seq. ID No. 104); TTT-GGA-CCA-CTC-TGT-GGC (Seq. ID No. 105); AAC-GGG-ATA-ACT-GCA-CCT (Seq. ID No. 106); TTT-GTG-GTT-TGT-GGT-GGA (Seq. ID No. 107); AGG-GAA-TAG-CTT-CAT-AGA (Seq. ID No. 108); ATC-ACG-AAG-AAG-GTT-CTG (Seq. ID

No. 109); CCG-AAG-ATG-TCT-TTG-GAA (Seq. ID No. 110); AAA-GAG-GTC-TAC-ATG-TCC (Seq. ID No. 111); TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115); ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116); GCA-CTT-ACC-GGC-CTA-AG (Seq. ID No. 117); CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118); ACA-GAA-CTA-AAC-CAT-CGT (Seq. ID No. 147); TAG-GCC-AGC-TTG-GAG-GAT (Seq. ID No. 148); CTA-GCT-GGG-AGG-ATT-T (Seq. ID No. 149); TGT-GCC-TCA-ACT-GAC-A (Seq. ID No. 150); TGC-TTT-GGG-ATG-TTT-CAA (Seq. ID No. 151); GCA-ATG-TCA-GAA-CTT-TTT-TC (Seq. ID No. 152); CCG-AAA-GAA-ATT-TGT-GGG (Seq. ID No. 153); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 154); TCA-AGG-CGA-TCG-AAA-TGT (Seq. ID No. 155); GAG-ACA-CAT-ATC-ACC-AAC (Seq. ID No. 156); CAG-AAA-TTT-CTT-TCG-GAT-A (Seq. ID No. 157); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 158); and AGC-CAA-AGG-AGT-TGA-ACA (Seq. ID No. 159) or the complement to any of the foregoing sequences and further provided that at least one probe comprises one of SEQ ID NOs 10-16 or the complement thereto.